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OM protein - protein search, using sw model

Run on: January 24, 2002, 09:08:13 ; Search time 23.82 Seconds
(without alignments)
410.482 Million cell updates/sec

Title: US-09-905-235-1

Perfect score: 675

Sequence: 1 MDAFVGTWKLVSSENFDDY.....KLVVECVMKGVSTRVYERA 132

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_1101.*
- 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
 - 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
 - 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
 - 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
 - 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
 - 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
 - 7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
 - 8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
 - 9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
 - 10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
 - 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
 - 12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
 - 13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
 - 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
 - 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
 - 16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
 - 17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
 - 18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
 - 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
 - 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
 - 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
 - 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	675	100.0	132	21	Human AFABP protei
2	625	92.6	132	21	Mouse AFABP protei
3	466	69.0	133	22	Mouse MDGI polypep
4	458	67.9	136	19	Human myelin P2 pr
5	453	67.1	131	12	MDGI active peptid
6	449	66.5	133	22	Human MDGI polypep
7	446	66.1	133	22	Bovine MDGI polypep
8	445	65.9	136	19	Bovine myelin P2 p
9	435.5	64.5	134	18	Porcine heart-fatt
10	399	59.1	132	18	Human cytoctatin I
11	399	59.1	132	19	Amino acid sequenc

12	399	59.1	132	19	AAW81106	Human cytoctatin I
13	399	59.1	132	20	AAW82403	Human 14-16 kDa FA
14	396	58.7	117	21	AAG03847	Human secreted pro
15	386.5	57.3	131	22	AAG66580	Human cytoctatin I
16	382	56.6	132	21	AAG03957	Human secreted pro
17	381	56.4	132	16	AAW73423	Mouse cellular x b
18	375	55.6	88	21	AAW58740	Breast and ovarian
19	366	54.2	135	15	AAW55866	Melanogenic inhibi
20	360	53.3	82	22	AAG75123	Human colon cancer
21	270	40.0	69	21	AAW65303	Human 5' EST relat
22	237	35.1	134	20	AAW68550	Human retinoid bin
23	229.5	34.0	133	16	AAW75643	Schistosoma mansoni
24	222	32.9	137	14	AAW42212	CRABP-I gene produ
25	210	31.1	56	21	AAG01405	Human secreted pro
26	201.5	29.9	138	14	AAW42211	CRABP-II gene prod
27	201.5	29.9	138	22	AAW76852	Human lung tumour
28	201.5	29.9	149	21	AAW58158	Lung cancer associ
29	194	28.7	99	21	AAW01603	Human secreted pro
30	186	27.6	160	21	AAW43403	Human cancer assoc
31	165	24.4	135	22	AAW38758	Human polypeptide
32	165	24.4	135	22	AAW60659	Human cellular ret
33	165	24.4	168	22	AAW40544	Human polypeptide
34	164	24.3	135	18	AAW30891	Human cytoctatin I
35	164	24.3	135	20	AAW32504	Human cytoctatin I
36	164	24.3	135	22	AAG66575	Human cytoctatin I
37	164	24.3	135	22	AAU02203	Retinol-binding pr
38	162	24.0	135	21	AAW92910	Human retinoid bin
39	136	20.1	156	22	AAU02202	Retinol-binding pr
40	122	18.1	107	18	AAW27561	Human cytoctatin I
41	122	18.1	107	18	AAW26581	Human cytoctatin I
42	122	18.1	107	20	AAW49535	Human cytoctatin I
43	122	18.1	107	20	AAW83929	Human growth inhib
44	115.5	17.1	106	22	AAG66579	Human cytoctatin I
45	110	16.3	55	9	AAW82557	Human cellular ret

ALIGNMENTS

RESULT 1
AAW90320
ID AAW90320 standard; Protein; 132 AA.
XX
AC AAW90320;
XX
DT 22-NOV-2000 (first entry)
XX
DE Human AFABP protein sequence.
XX
KW AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion;
KW lesion formation inhibition; macrophage; adipocyte; atherosclerosis;
KW serum cholesterol; therapy; human.
XX
OS Homo sapiens.
XX
PN WO200047734-A1.
XX
PD 17-AUG-2000.
XX
PF 11-FEB-2000; 2000WO-US03560.
XX
PR 12-FEB-1999; 99US-0119880.
PA (HARD) HARVARD COLLEGE.
PI Lee M, Perrella MA, Hotamisligil GS;
DR WPI; 2000-506094/45.
DR N-PSDB; AAA37717.
XX
PT Reducing expression of adipocyte fatty acid binding protein through
PT administration of a compound is used to inhibit formation of an
PT atherosclerotic lesion.

XX Disclosure; Page 14; 43pp; English.

XX This sequence represents the human AFABP (adipocyte fatty acid binding protein) protein sequence. The invention relates to a method for inhibiting formation of an atherosclerotic lesion comprising administering to a mammal a compound that reduces expression of adipocyte fatty acid binding protein (AFABP). The method is used to inhibit formation of atherosclerotic lesions. The method is used to identify compounds which can be used to inhibit formation of atherosclerotic lesions through inhibition of AFABP binding to an intracellular ligand in a macrophage or adipocyte, inhibition of development of an atherosclerotic lesion, inhibition of a macrophage differentiating into a foam cell or inhibition of AFABP expression in a cell. AFABP activity may be inhibited to treat atherosclerosis or to treat individuals at risk of developing atherosclerosis. Inhibiting AFABP expression or activity reduces the development of atherosclerotic lesions despite a high level of serum cholesterol.

XX Sequence 132 AA;

Query Match 100.0%; Score 675; DB 21; Length 132;
 Best Local Similarity 100.0%; Pred. No. 4.2e-71;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCDAPVGTWKLVSSENFDDYKKEVGVGFPATRKVAGMAPNMIISVNGDVITIKSESTFKN 60
 Db 1 mcdafvgtwklvssefddymkevvgvfatrkvagmapnmlisvngdvtiksestfkn 60
 Qy 61 TEISFILGOEFDEVTDADRKKVKTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
 Db 61 teisfilgofdevtdadrkvvkstltldggvlvvhvqvwgdkgsttikrkrddklvvevcvm 120
 Qy 121 KGVTSRYVERA 132
 Db 121 kgvtstryvera 132

RESULT 2
 AAY90319
 ID AAY90319 standard; Protein; 132 AA.

XX AC AAY90319;
 XX DT 22-NOV-2000 (first entry)
 XX DE Mouse AFABP protein sequence.
 XX KW AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion;
 KW lesion formation inhibition; macrophage; adipocyte; atherosclerosis;
 KW serum cholesterol; therapy; mouse.
 XX OS Mus sp.
 XX PN WO200047734-A1.
 XX PD 17-AUG-2000.
 XX PF 11-FEB-2000; 2000WO-US03560.
 XX PR 12-FEB-1999; 99US-0119880.
 XX PA (HARD) HARVARD COLLEGE.
 XX PI Lee M, Perrella MA, Rotamisligil GS;
 XX WPI; 2000-506094/45.
 XX DR N-PSDB: AAA37716.
 XX Reducing expression of adipocyte fatty acid binding protein through administration of a compound is used to inhibit formation of an atherosclerotic lesion.

XX Disclosure; Page 14; 43pp; English.

XX This sequence represents the mouse AFABP (adipocyte fatty acid binding protein) protein sequence. The invention relates to a method for inhibiting formation of an atherosclerotic lesion comprising administering to a mammal a compound that reduces expression of adipocyte fatty acid binding protein (AFABP). The method is used to inhibit formation of atherosclerotic lesions. The method is used to identify compounds which can be used to inhibit formation of atherosclerotic lesions through inhibition of AFABP binding to an intracellular ligand in a macrophage or adipocyte, inhibition of development of an atherosclerotic lesion, inhibition of a macrophage differentiating into a foam cell or inhibition of AFABP expression in a cell. AFABP activity may be inhibited to treat atherosclerosis or to treat individuals at risk of developing atherosclerosis. Inhibiting AFABP expression or activity reduces the development of atherosclerotic lesions despite a high level of serum cholesterol.

XX Sequence 132 AA;

Query Match 92.6%; Score 625; DB 21; Length 132;
 Best Local Similarity 91.7%; Pred. No. 2.9e-65;
 Matches 121; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MCDAPVGTWKLVSSENFDDYKKEVGVGFPATRKVAGMAPNMIISVNGDVITIKSESTFKN 60
 Db 1 mcdafvgtwklvssefddymkevvgvfatrkvagmapnmlisvngdvtirsetfkn 60
 Qy 61 TEISFILGOEFDEVTDADRKKVKTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
 Db 61 teisfilgofdevtdadrkvvkstltldggvlvvhvqvwgdkgsttikrkrddklvvevcvm 120
 Qy 121 KGVTSRYVERA 132
 Db 121 kgvtstryvera 132

RESULT 3
 AAG66576
 ID AAG66576 standard; Protein; 133 AA.

XX AC AAG66576;
 XX DT 22-OCT-2001 (first entry)
 XX DE Mouse MDGI polypeptide.
 XX KW Mouse; cytoostatin III; cytoostatic; epithelial cell growth;
 KW milk production; breast involution; cardiac myocyte hypertrophy;
 KW leukaemia; MDGI; mammary-derived growth inhibitor.
 XX OS Mus sp.
 XX PN US6232291-B1.
 XX PD 15-MAY-2001.
 XX PF 10-MAY-1999; 99US-0307817.
 XX PR 19-MAR-1996; 96US-0013655.
 XX PR 19-MAR-1997; 97US-0820825.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Ni J, Yu G, Gentz R, Dillon PJ;
 XX WPI; 2001-342775/36.
 XX Cytostatin III polypeptides that modulate growth of epithelial cells, stimulate milk production in humans and cows and promote involution of breast, for research, biological, clinical and therapeutic purposes.

XX		Disclosure; Fig 2; 3lpp; English.
XX		The invention relates to an isolated Cytostatin III polypeptide comprising a sequence selected from amino acids 1-135, 2-135, 108-135,
CC		129-135 and 118-125, of a sequence of 135 amino acids fully defined in
CC		the specification. The polypeptide is useful for modulating growth of
CC		epithelial cells, for stimulating milk production in humans and cows,
CC		and for promoting involution of breasts. It is also useful for treating
CC		cardiac myocyte hypertrophy and leukaemia, and is useful for research,
CC		and biological, clinical and therapeutic purposes. The present
CC		sequence is provided in the specification for comparison studies
CC		with human cytochrome III.
XX	SQ	Sequence 133 AA;
Query Match	69.0%; Score 466; DB 22; Length 133;	
Best Local Similarity	67.94; Pred. No. 1.le-46;	
Matches	89; Conservative 15; Mismatches 27; Indels 0; Gaps 0;	
QY	1 MCDAFVGFWKLVSSNFDDYMKEVGVGFATRKVAGMAKPNNMIIISVNGDVIITIKSESTFKN 60 : : : :	
Dd	1 madafvgtwklvdknfadymksgvgfatrqvasmtpttlliekngdtitktgstfkn 60 : : : : : :	
QY	61 TEISFILGQEDEVTAADRRKYVKSTITLDGGVLHVHQRWDGSKTTTIKKREDDKLVECVCM 120 : : : : : :	
Dd	61 teinfqlgiefdevtaddarkvkksvltdggklihvqkwnggettltrelvdgkkiltith 120 : : : : : :	
QY	121 KGVISTRVRYER 131 :	
Dd	121 gsvvstrtyek 131 :	
RESULT 4		
AAW40227		
ID	AAW40227 standard; Protein; 136 AA.	
AC	AAW40227;	
XZ		
DT*	26-JUN-1998 (first entry)	
XX	Human myelin P2 protein.	
DE		
KW	Human; myelin; p2 protein; treatment; inflammatory polyneuritis; Guillain-Barre syndrome; vasculitis; nerve inflammation; gammapathy.	
OS	Homo sapiens.	
FH	Key Location/Qualifiers	
FT	Misc-difference 49 /note= "encoded by AAT"	
PX	WO9803647-A2.	
PD	29-JAN-1998.	
PF	18-JUL-1997; 97WO-DEO1535.	
PR	18-JUL-1996; 96DE-1029095.	
(GOLD/) GOLD R. (WEIS/) WEISHAUP T A.		
GOLD R, Weishaupt A;		
WIPI; 1998-120772/11.		
N-PSDB; AAVI0405.		
Recombinant myelin proteins for treating T-cell mediated disease of peripheral nervous system - by high dose antigen therapy, causing apoptosis in T cells, for treating e.g. polyneuritis or		

CC AAR13561 are used for the production of antibodies. These are used to
CC study the mechanism of action of MDGI and related proteins and to
CC identify new regulators active in the same way.
CC The peptides are synthesised by usual chemical methods and coupled
CC to a carrier. The resulting conjugate is used to immunise animals
CC and recovered sera tested for reactivity against antigens
CC immobilised on nitrocellulose.

XX Sequence 131 AA;

Query Match 67.1%; Score 453; DB 12; Length 131;
Best Local Similarity 67.4%; Pred. No. 3.7e-45;
Matches 87; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 3 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPMIISVNGDVITIKSESTFKNTE 62
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 2 dafvgtwklvsseinfddymksglvgvfatrgvgnmtkptliisvngdtvliktgstfknte 61

QY 53 ISFILGQEFDEVTDADRKKVSTITLDGGLVHVQKWDGKSTTIKKREDDDKLVECVMKG 122
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 62 isfilgvefdettaddrkksivtldggklvgvqkwngqetslvremvdgklliltlthgt 121

QY 123 VTSTRVYER 131
|||||

Db 122 avctrvyek 130
|||||

RESULT 6

AAG66578
ID AAG66578 standard; Protein; 133 AA.

XX AAG66578;

DT 22-OCT-2001 (first entry)

XX Human MDGI polypeptide.

XX Human; cytostatin III; cytostatic; epithelial cell growth;
KW milk production; breast involution; cardiac myocyte hypertrophy;
KW leukaemia; MDGI; mammary-derived growth inhibitor.

OS Homo sapiens.

XX US6232291-B1.

XX 15-MAY-2001.

XX 10-MAY-1999; 99US-0307817.

XX 19-MAR-1996; 96US-0013655.

XX 19-MAR-1997; 97US-0820825.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Yu G, Gentz R, Dillon PJ;

XX WPI; 2001-342775/36.

XX Cytostatin III polypeptides that modulate growth of epithelial cells,
PT stimulate milk production in humans and cows and promote involution of
PT breast, for research, biological, clinical and therapeutic purposes -

XX Disclosure; Fig 2; 3lpp; English.

XX The invention relates to an isolated Cytostatin III polypeptide
CC comprising a sequence selected from amino acids 1-135, 2-135, 108-135,
CC 129-135 and 118-125, of a sequence of 135 amino acids fully defined in
CC the specification. The polypeptide is useful for modulating growth of
CC epithelial cells, for stimulating milk production in humans and cows,
CC and for promoting involution of breasts. It is also useful for treating
CC cardiac myocyte hypertrophy and leukaemia, and is useful for research,
CC and biological, clinical and therapeutic purposes. The present

CC sequence is provided in the specification for comparison studies
CC with human cytostatin III.

XX Sequence 133 AA;

Query Match 66.5%; Score 449; DB 22; Length 133;
Best Local Similarity 64.9%; Pred. No. 1.1e-44;
Matches 85; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

QY 1 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPMIISVNGDVITIKSESTFKN 60
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 1 mvdafvgtwklvsseinfddymksglvgvfatrgvsmctkptliiekngdiltkchstfkn 60

QY 61 TEISFILGQEFDEVTDADRKKVSTITLDGGLVHVQKWDGKSTTIKKREDDDKLVECVCM 120
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 61 teisfilgvefdettaddrkksivtldggklvhlgkwdggettlvrelidgklliltlth 120

QY 121 KGVSTRVYER 131
|||||

Db 121 gtavctrvyek 131
|||||

RESULT 7

AAG66577
ID AAG66577 standard; Protein; 133 AA.

XX AAG66577;

DT 22-OCT-2001 (first entry)

XX Bovine MDGI polypeptide.

XX Bovine; cytostatin III; cytostatic; epithelial cell growth;
KW milk production; breast involution; cardiac myocyte hypertrophy;
KW leukaemia; MDGI; mammary-derived growth inhibitor.

OS Bos sp.

XX US6232291-B1.

XX 15-MAY-2001.

XX 10-MAY-1999; 99US-0307817.

XX 19-MAR-1996; 96US-0013655.

XX 19-MAR-1997; 97US-0820825.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Yu G, Gentz R, Dillon PJ;

XX WPI; 2001-342775/36.

XX Cytostatin III polypeptides that modulate growth of epithelial cells,
PT stimulate milk production in humans and cows and promote involution of
PT breast, for research, biological, clinical and therapeutic purposes -

XX Disclosure; Fig 2; 3lpp; English.

XX The invention relates to an isolated Cytostatin III polypeptide
CC comprising a sequence selected from amino acids 1-135, 2-135, 108-135,
CC 129-135 and 118-125, of a sequence of 135 amino acids fully defined in
CC the specification. The polypeptide is useful for modulating growth of
CC epithelial cells, for stimulating milk production in humans and cows,
CC and for promoting involution of breasts. It is also useful for treating
CC cardiac myocyte hypertrophy and leukaemia, and is useful for research,
CC and biological, clinical and therapeutic purposes. The present
CC sequence is provided in the specification for comparison studies
CC with human cytostatin III.

XX Sequence 133 AA;

Query Match 59.1%; Score 399; DB 18; Length 132;
Best Local Similarity 56.8%; Pred. No. 7.6e-39;
Matches 75; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

[illegible]

RESULT 11.
AAW80949
ID AAW80949 standard; Protein; 132 AA.
XX
AC AAW80949;

RESULT	11
AAW80949	
ID	AAW80949 standard; Protein; 132 AA.
XX	
AC	AAW80949;
AC	
DT	16-FEB-1999 (first entry)
DT	
XX	
DE	Amino acid sequence of the human fatty acid binding protein.
XX	
XX	Human; fatty acid binding protein; Hu-FABP; developmental disorder;
KW	cancer; spina bifida; hydrocephalus; hereditary neuropathy;
KW	Charcot-Marie-Tooth disease; neurofibromatosis; antagonist;
KW	hyperaldosteronism; adenocarcinoma.
XX	
OS	Homo sapiens.
OS	
XX	WO9845440-A1.
PN	
XX	
PD	15-OCT-1998.
XX	
PF	08-APR-1998; 98WO-US07084.
XX	
PR	08-APR-1997; 97US-0825783.
XX	
PA	(INCY-) INCYTE PHARM INC.
XX	
PI	Hillman JL, Shah P;
XX	
DR	WPI; 1998-594484/50.
DR	N-PSDB; AAW68587.
XX	
PT	New isolated human fatty acid binding protein - used to develop
PT	products for treating, e.g. spina bifida, anaemia, glaucoma, seizure
PT	disorders, epilepsy and cerebrovascular disease
XX	
PS	Claim 1; Fig 1; 59pp; English.
XX	
CC	This is the amino acid sequence of the human fatty acid binding
CC	protein (Hu-FABP) used in the method of the invention. The Hu-FABP
CC	plays a role in developmental disorders and cellular development and
CC	differentiation, including cancers. The Hu-FABP can be used for
CC	treating developmental disorders, e.g. spina bifida, hydrocephalus,
CC	and hereditary neuropathies such as Charcot-Marie-Tooth disease and
CC	neurofibromatosis. Antagonists to the Hu-FABP can be used for
CC	treating a disorder associated with cellular development and
CC	differentiation, e.g. hyperaldosteronism, and cancers including

CC adenocarcinoma, in particular, cancers of neurological origin such as
 CC cancers of the breast and kidney. The products can also be used for
 CC detection, diagnosis and drug screening.
 XX
 SQ Sequence 132 AA;

Query Match 59.1%; Score 399; DB 19; Length 132;
 Best Local Similarity 56.8%; Pred. No. 7.6e-39;
 Matches 75; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

QY 1 MCDAFVGTWKLVSSENFDDYMKVGVGATRKVAGMAKPMNIISVNGDVITIKSESTFKN 60
 Db 1 mveafcatwkltnsqnfdeymkalgvgfatrgvntkptvilsqegdkvvtlftstfkn 60
 QY 61 TEISFILGOEFDEVTDADRKVKSTITLDGVLVHVQKWDGKSTTIKKRREDDKLVVECV 120
 Db 61 teisfqlgeefdettdaddrncksvvslgdgklvhlqkwdgktnfvrelkgdkmvtltf 120
 QY 121 KGVSTRYVERA 132
 Db 121 gdvavvrhyeka 132

RESULT 12
 AAW81106
 ID AAW81106 standard; Protein; 132 AA.
 AC AAW81106;
 DT 29-JAN-1999 (first entry)
 DE Human cytostatin II.
 KW Human; cytostatin; cell growth; tumour; nervous system;
 KW viral infection; microbial infection.
 OS Homo sapiens.
 XX WO9844109-A1.
 XX 08-OCT-1998.
 XX 25-MAR-1998; 98WO-US05839.
 XX 27-MAR-1997; 97US-0041645.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (LONG-) LONG ISLAND JEWISH MEDICAL CENT.
 XX Gentz RL, Nardelli B, Ni J, Shi YE, Yu G;
 WPI: 1998-557110/47.
 DR N-PSDB; AAV68225.
 XX
 PT New isolated human cytostatin II - used to develop products for the
 PT treatment of e.g. cancers or viral or microbial infections or for
 PT protecting nervous system cells from toxic agents
 XX
 PS Claim 1; Fig 1; 73pp; English.

CC The nucleotide sequence encoding Human cytostatin can inhibit cell growth
 CC and modulate differentiation. The cytostatin II polypeptides can be used
 CC for inhibiting tumour growth in a subject, for stimulating growth of or
 CC protecting nervous system cells from toxic agents or for protecting
 CC against or treating viral or microbial infections in mammals. The
 CC products can also be used e.g. to modulate angiogenesis, to modulate
 CC breast development and milk production. They can also be used in
 CC cerebellar granular cells and photo receptor cells to provide protection
 CC from lipid peroxidation associated with the oxidative stress induced
 CC during early stages of ischemia, apoptosis, and excitatory amino acid
 CC induced cell death. The retinoid binding potential of cytostatin II
 CC may be used on photo receptor cells in vivo or in vitro. The activity of

CC haematopoiesis indicates a possible immunosuppressive activity or a
 CC lineage specific stimulation of haematopoiesis which could be used for
 CC treating conditions requiring immunosuppression. Antagonists to
 CC cytosatin II may be used in vivo to induce deficiencies or enhancement
 CC in the immune or in the haematopoietic systems. They may be used e.g. to
 CC treat cardiac myocyte hypertrophy or leukemia.
 XX
 SQ Sequence 132 AA;

Query Match 59.1%; Score 399; DB 19; Length 132;
 Best Local Similarity 56.8%; Pred. No. 7.6e-39;
 Matches 75; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

QY 1 MCDAFVGTWKLVSSENFDDYMKVGVGATRKVAGMAKPMNIISVNGDVITIKSESTFKN 60
 Db 1 mveafcatwkltnsqnfdeymkalgvgfatrgvntkptvilsqegdkvvtlftstfkn 60
 QY 61 TEISFILGOEFDEVTDADRKVKSTITLDGVLVHVQKWDGKSTTIKKRREDDKLVVECV 120
 Db 61 teisfqlgeefdettdaddrncksvvslgdgklvhlqkwdgktnfvrelkgdkmvtltf 120
 QY 121 KGVSTRYVERA 132
 Db 121 gdvavvrhyeka 132

RESULT 13
 AAW82403
 ID AAW82403 standard; Protein; 132 AA.
 AC AAW82403;
 DT 23-FEB-1999 (first entry)
 DE Human 14-16 kDa FABP analogue GEN 128B10 protein.
 KW FABP; detection; gene expression; analogue; GEN 128B10.
 OS Homo sapiens.
 XX JPI0286089-A.
 XX 27-OCT-1998.
 XX 15-APR-1997; 97JP-0096908.
 XX 15-APR-1997; 97JP-0096908.
 XX (SAKA) OTSUKA PHARM CO LTD.
 XX WPI: 1999-063481/06.
 DR N-PSDB; AAV73482, AAV73483.
 XX
 PT New human rab7GFP-combined analogous protein gene - useful for
 PT detection of its expression in tissues
 XX
 PS Example 3; Page 24; 35pp; Japanese.
 XX
 CC This sequence represents a novel human 14-16 kDa FABP protein analogue,
 CC GEN 128B10. The gene is useful for the detection of gene expression in
 CC various tissues.
 XX
 SQ Sequence 132 AA;

Query Match 59.1%; Score 399; DB 20; Length 132;
 Best Local Similarity 56.8%; Pred. No. 7.6e-39;
 Matches 75; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

QY 1 MCDAFVGTWKLVSSENFDDYMKVGVGATRKVAGMAKPMNIISVNGDVITIKSESTFKN 60
 Db 1 mveafcatwkltnsqnfdeymkalgvgfatrgvntkptvilsqegdkvvtlftstfkn 60

QY	61	TEISFILGQFDEVTADDRKVKSTITLDGGVLVHVQKWGCKSTTIKRREDDKLIVVECV	120
		: : : : :	
Dd	61	teisfqlgeifdetdrackrvssvldgklvhlgkdgktefnvreikdgkmvmtltf	120
QY	121	KGVSTRVYERA 132	
		: : : :	
Dd	121	gdvvavrhnyeka 132	

RESULT 14

AAG03847

ID AAG03847 standard; Protein; 117 AA.

XX AC AAG03847;

XX DT 06-OCT-2000 (first entry)

XX DE Human secreted protein, SEQ ID NO: 7928.

XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

XX KW gene therapy; chromosome mapping.

XX OS Homo sapiens.

XX PN EP1033401-A2.

XX PD 06-SEP-2000.

XX PF 21-FEB-2000; 2000EP-0200610.

XX PR 26-FEB-1999; 99US-0122487.

XX PA (GEST) GENSET.

XX PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX N-PSDB; AAC03853.

XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for

XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX PS Claim 13; SEQ ID 7928; Tippet + CD-ROM; English.

XX CC The present sequence is a polypeptide encoded by one of a large number

CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs

CC were prepared from total human RNAs or polyA+ RNAs derived from 30

CC different tissues. EST sequences usually correspond mainly to the 3'

CC untranslated region (UTR) of the mRNA because they are often obtained

CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for

CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in

CC those cases where longer cDNA sequences have been obtained, the full 5'

CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'

CC ends and can therefore be used to obtain full length cDNAs and genomic

CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and

CC chromosome mapping procedures. They are used to obtain upstream

CC regulatory sequences and to design expression and secretion vectors.

XX SQ Sequence 117 AA;

Query Match	58.7%;	Score 396;	DB 21;	Length 117;
Best Local Similarity	59.1%;	Pred. No. 1.4e-38;		
Matches	76;	Conservative 13;	Mismatches 21;	Indels 0; Gaps

QY	1	MCDAFGVTGLVSENFDYMKVGVFATRKVAGMAKNMIIISVNGDVTIKSESTFN	60
		: : : : : :	
Dd	1	msnflgtwklvsenfdyymkalvglatrkignlakptviskkqdiitrtstfk	60

QY	61	TEISFILGQFDEVTADDRKVKSTITLDGGVLVHVQKWGCKSTTIKRRE	110
		: :	

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Db		1	MADAFVGTWKLVDLSKFNDDYMSLGVGFATQVASHMTKTPTTILIEKNGDITIKTKQSTFNN	60
QY		61	TEISFILGQFFDEVTDADDRKVKSTIYLDGGVLHVHOKWGDKSTTIKRREDDKLVVECYM	120
			: : : : : :	
Db		61	TEINFOLGIEFEVTADDRKVKSLVTDGGKLIHVKWNGQETTLTRELYDGLKIILLTH	120
QY		121	KGYTSTRVRYER	131
Db		121	GSVVSTRVYEK	131

RESULT 2
US-08-470-298B-7
Sequence 7, Application US/08470298B
Patent No. 5844081
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: YU, GUO-LIANG
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: CYTOSTATIN I
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850

Query Match	69.0%;	Score 466;	DB 2;	Length 131;
Best Local Similarity	67.9%;	Pred. NO. 5.3e-49;		
Matches	89;	Conservative 15;	Mismatches 27;	Indels 0; Gaps
Qy	1	MCDAFVCTWKLVSSEFDDYMKVGVCFATPKVAGMAKPKMIISVNGDVTIKSESTFKN	60	
Db	1	MADAFVCTWKLVSNSKFNDDYMKSLGVGFATPKQVASMTPKTTIEKNGDITIIKTQSTFKN	60	
Qy	61	TEISFILGQBFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVCVCM	120	
Db	61	TEINFQLGIEFEVTADDRKVSIVLTDGGKLIHVQKNGQETTLRELVDGKLILTLH	120	
Qy	121	KGVTSTRVYER	131	
Db	121	GSVVSTRTYEK	131	

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RESULT      3
US-08-820-825-11
; Sequence 11, Application US/08820825
; Patent No. 5945309
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRES:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,825
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-825-11

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Query Match          69.0%; Score 466; DB 2; Length 133;
Best Local Similarity 67.9%; Pred. No. 5.4e-49;
Matches 89; Conservative 15; Mismatches 27; Indels 0; Gaps
120

Qy      1  MCDAFVGTWKLVSSENEDDYMKVGVGFATPKYAGNAKPMILSVNGDVTIKSESTFKN 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  MADAFVGTWKLVDKSNFDDYMKSLGVGFATPQVASMTPKPTIIKNGDITTIKTQSTFKN 60

Qy      61 TEISFIILGQGFDEVTADBRVKSTFTILDGVLVHVOKWDGKSTTKRKREDDKLVVYECVM 120
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 TEINFQIGIEFDEVTADBRKVSFLYLDGGKLIHVQWNGQETTLRELVDGKLIITLTH 120

Qy      121 KGVSTRWYER 131
      | | | | |
Db      121 GSVVSTRYEK 131

RESULT      4
US-09-023-073A-7
; Sequence 7, Application US/09023073A
; Patent No. 5977309
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11

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Qy	1	MCDA	FGT	WKL	VSS	NFDD	YMK	EVG	VFAT	RVAG	MAK	PNN	II	SVN	CDV	IT	KSE	ST	FKN	60	
		-	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	
Db	1	MSN	FLG	TWK	LVS <td>NFDD</td> <td>YMK</td> <td>ALG</td> <td>VGL</td> <td>ATR</td> <td>KLGN</td> <td>LAK</td> <td>PV</td> <td>II</td> <td>SKG</td> <td>DI</td> <td>IT</td> <td>RT <td>EST <td>FKN <td>60</td> </td></td></td>	NFDD	YMK	ALG	VGL	ATR	KLGN	LAK	PV	II	SKG	DI	IT	RT <td>EST <td>FKN <td>60</td> </td></td>	EST <td>FKN <td>60</td> </td>	FKN <td>60</td>	60


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CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,731A
FILING DATE: 24-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Robert H
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PF175
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-409-731A-10

Query Match          66.5%; Score 449; DB 1; Length 133;
Best Local Similarity 64.9%; Pred. No. 6.3e-47;
Matches 85; Conservative 16; Mismatches 30; Indels 0; Gaps 0

QY      1 MCDAFYGTWKLVSSENFDDYMKVGVGFATRKVAGNAKPNMIISVNGDVITIKSESTFKN 60
        | ||| ||||| :||||| :|||||:| || || |||||:| |||||
DB      1 MVDAFLGTWLVDLSKNFDYDKSLGSGVFATRQVASMTKPTTIEKNGDILTLLKTHSTFKN 60

QY      61 TEISFILQGFEDEVTDADDRVKVTIILDGGLVHVHVKWGSKSTTIKRREDKLVVECYM 120
        ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      61 TEISFKLGVEFDETTADDRVKKSIVTLDGGLVHLQKWDGQETTLRELIDGLLTLPLH 120

QY      121 KGVTSRTVRYER 131
        || |||
DB      121 GTAVCTRTYEK 131

RESULT 12
US-08-470-298B-10
Sequence 10, Application US/08470298B
Patent No. 5844081
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: YU, GUO-LIANG
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: CYTOSTATIN I
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,298B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ALLAN A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF175D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8512
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: FARP (FIGURE 2)
; US-08-470-298B-10

Query Match 66.5%; Score 449; DB 2; Length 133;
Best Local Similarity 64.9%; Pred. No. 6.3e-47;
Matches 85; Conservative 16; Mismatches 30; Indels 0; Gaps

QY 1 MCDAFVCTWKLVSSENFDDYMKVGVGFAPRKVAGAKPMIILSVNGDVITIKSESTFKN 60
DB 1 MVDAPLGTWKLVDKSNFDDTKSLGSLGVGFAPRVQVSWTKPTTITEKNGDILTLKTHSTFRN 60

QY 61 TEISFILGQEFDEVTADRRKVKSTITIDGGVLVHVQKWDGCKSTTIKRRKREDDKLKLVVECYM 120
DB 61 TEISFKLGVEFDETTADRRKVKSVITLDGGKLVLQKWDQGETTLVRELIDGKLILTLTH 120

QY 121 KGVYSTRVYER 131
DB 121 GTAVCTRTYEK 131

RESULT 13
US-08-820-825-13
; Sequence 13, Application US/08220825
; Patent No. 5945309
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK
; TITLE OF INVENTION: CYTOSTATIN III
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,825
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF222
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504

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Db 61 TEISFKLGVEFDETTADDRKVKSIVTLDGGKLVHLQKWQDQETTLLVRELIDGKLLTLTH 120
Qy 121 KGVISTRYER 131
|| ||:
Db 121 GTAVCTRYEK 131

Search completed: January 24, 2002, 09:15:40
Job time: 382 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2002, 09:14:28 ; Search time 97.19 Seconds
(without alignments)
377.104 Million cell updates/sec

Title: US-09-905-235-1

Perfect score: 675

Sequence: 1 MCDFAVGTWKLVSSENFDDY.....KLVVECMVKGVTSRIVYERA 132

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /cgn2_6/ptodata/2/paa/US099_COMB.pcp.*
24: /cgn2_6/ptodata/2/paa/US60_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	100.0	132	17	US-09-391-053-1
2	675	100.0	132	17	US-09-391-053A-1
3	675	100.0	132	19	US-09-503-596-4
4	675	100.0	132	23	US-09-905-235-1
5	675	100.0	136	21	US-09-760-469-913
6	675	100.0	136	21	US-09-760-469-915
7	675	100.0	136	21	US-09-760-469-917
8	675	100.0	136	21	US-09-760-469-1429
9	675	100.0	136	21	US-09-760-469-1432

10	675	100.0	136	21	US-09-760-469-1433
11	675	100.0	136	21	US-09-760-469-1434
12	649	96.1	129	22	US-09-834-366-17169
13	649	96.1	129	22	US-09-834-366-17169
14	625	92.6	132	19	US-09-503-596-5
15	572	84.7	132	20	US-09-699-146-172
16	507	75.1	157	24	US-09-212-664-606
17	488	72.3	97	16	US-09-216-665-18
18	467	69.0	133	12	US-08-825-783-6
19	466	69.0	131	1	PCT-US96-03697-11
20	466	69.0	131	14	US-09-023-073-7
21	466	69.0	133	1	PCT-US96-01640-7
22	466	69.0	133	8	US-08-470-298A-7
23	466	69.0	133	21	US-09-734-036-11
24	463	68.6	132	1	PCT-US96-01640-11
25	463	68.6	132	8	US-08-470-298A-11
26	463	68.6	132	14	US-09-023-073-11
27	463	68.6	132	22	US-09-834-366-15504
28	463	68.6	138	24	US-09-197-873-15504
29	463	68.6	141	21	US-09-760-469-903
30	463	68.6	141	21	US-09-760-469-1419
31	449	66.5	133	1	PCT-US96-01640-10
32	449	66.5	133	1	PCT-US96-03697-13
33	449	66.5	133	8	US-08-470-298A-10
34	449	66.5	133	12	US-08-825-783-7
35	449	66.5	133	14	US-09-023-073-10
36	449	66.5	133	21	US-09-734-036-13
37	449	66.5	133	23	US-09-948-941-307
38	449	66.5	137	21	US-09-760-469-910
39	449	66.5	137	23	US-09-948-941-358
40	446	66.1	133	21	US-09-734-036-12
41	437	64.7	138	20	US-09-699-146-173
42	430.5	63.8	132	1	PCT-US96-03697-12
43	428	63.4	141	21	US-09-758-471-3729
44	417	61.8	105	22	US-09-834-366-14769
45	417	61.8	105	24	US-09-197-873-14769

ALIGNMENTS

RESULT 1
US-09-391-053-1
; Sequence 1, Application US/09391053
; GENERAL INFORMATION:
; APPLICANT: Robt, Jeffrey A.
; APPLICANT: Biller, Scott A.
; APPLICANT: Jacobson, Bruce L.
; APPLICANT: Parker, Rex A.
; APPLICANT: Jamil, Haris
; APPLICANT: Kodukula, Krishna
; TITLE OF INVENTION: METHOD FOR TREATING DIABETES EMPLOYING AN AP2 INHIBITOR
; TITLE OF INVENTION: AND COMBINATION
; FILE REFERENCE: LA24aSequenceListing
; CURRENT APPLICATION NUMBER: US/09/391,053
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: 60/100,677
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-053-1

Query Match 100.0%; Score 675; DB 17; Length 132;
Best Local Similarity 100.0%; Pred. No. 2,1e-67;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCDFAVGTWKLVSSENFDDYKVGVFATRKVAGMAKPNMILSVNGDVITIKSESTFKN 60
|||||

Db 1 MDAFVGTVKLVSSNFDDYMKVGVGFPATRKVAGMAKPNNMIISVNGDVITIKSESTFKN 60
Qy 61 TEISFILGOEFDEVTAADRKKVKSITITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
Db 61 TEISFILGOEFDEVTAADRKKVKSITITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
Qy 121 KGVTSRTRYERA 132
Db 121 KGVTSRTRYERA 132

RESULT 2
US-09-391-053A-1
; Sequence 1, Application US/09391053A
; GENERAL INFORMATION:
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
; TITLE OF INVENTION: METHOD FOR TREATING DIABETES EMPLOYING AN AP2 INHIBITOR AND COM
; FILE REFERENCE: LA24a
; CURRENT APPLICATION NUMBER: US/09/391,053A
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 132
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-391-053A-1

Query Match 100.0%; Score 675; DB 17; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-67;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDAFVGTVKLVSSNFDDYMKVGVGFPATRKVAGMAKPNNMIISVNGDVITIKSESTFKN 60
Db 1 MDAFVGTVKLVSSNFDDYMKVGVGFPATRKVAGMAKPNNMIISVNGDVITIKSESTFKN 60
Qy 61 TEISFILGOEFDEVTAADRKKVKSITITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
Db 61 TEISFILGOEFDEVTAADRKKVKSITITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
Qy 121 KGVTSRTRYERA 132
Db 121 KGVTSRTRYERA 132

RESULT 3
US-09-503-596-4
; Sequence 4, Application US/09503596
; GENERAL INFORMATION:
; APPLICANT: Lee et al.
; TITLE OF INVENTION: Inhibiting formation of Artherosclerotic Lesions
; FILE REFERENCE: 21509-042
; CURRENT APPLICATION NUMBER: US/09/503,596
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/119,880
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-503-596-4

Query Match 100.0%; Score 675; DB 19; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-67;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDAFVGTVKLVSSNFDDYMKVGVGFPATRKVAGMAKPNNMIISVNGDVITIKSESTFKN 60
Db 1 MDAFVGTVKLVSSNFDDYMKVGVGFPATRKVAGMAKPNNMIISVNGDVITIKSESTFKN 60

Qy 61 TEISFILGOEFDEVTAADRKKVKSITITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
Db 61 TEISFILGOEFDEVTAADRKKVKSITITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
Qy 121 KGVTSRTRYERA 132
Db 121 KGVTSRTRYERA 132

RESULT 4
US-09-905-235-1
; Sequence 1, Application US/09905235
; GENERAL INFORMATION:
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
; TITLE OF INVENTION: METHOD FOR TREATING DIABETES EMPLOYING AN AP2 INHIBITOR AND CO
; FILE REFERENCE: LA24a
; CURRENT APPLICATION NUMBER: US/09/905,235
; CURRENT FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 132
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-905-235-1

Query Match 100.0%; Score 675; DB 23; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.1e-67;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDAFVGTVKLVSSNFDDYMKVGVGFPATRKVAGMAKPNNMIISVNGDVITIKSESTFKN 60
Db 1 MDAFVGTVKLVSSNFDDYMKVGVGFPATRKVAGMAKPNNMIISVNGDVITIKSESTFKN 60
Qy 61 TEISFILGOEFDEVTAADRKKVKSITITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
Db 61 TEISFILGOEFDEVTAADRKKVKSITITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
Qy 121 KGVTSRTRYERA 132
Db 121 KGVTSRTRYERA 132

RESULT 5
US-09-760-469-913
; Sequence 913, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ54
; CURRENT APPLICATION NUMBER: US/09/760,469
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 913
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-469-913

Query Match 100.0%; Score 675; DB 21; Length 136;
Best Local Similarity 100.0%; Pred. No. 2.2e-67;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDAFVGTVKLVSSNFDDYMKVGVGFPATRKVAGMAKPNNMIISVNGDVITIKSESTFKN 60
Db 5 MDAFVGTVKLVSSNFDDYMKVGVGFPATRKVAGMAKPNNMIISVNGDVITIKSESTFKN 64
Qy 61 TEISFILGOEFDEVTAADRKKVKSITITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120

Db 65 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECVM 124
|||||

QY 121 KGVSTRVYERA 132
|||||
Db 125 KGVSTRVYERA 136
|||||

RESULT 6

US-09-760-469-915
; Sequence 915, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254
; CURRENT APPLICATION NUMBER: US/09/760,469
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 915
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-469-915

Query Match 100.0%; Score 675; DB 21; Length 136;
Best Local Similarity 100.0%; Pred. No. 2.2e-67;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
|||||
Db 5 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 64
|||||

QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECVM 120
|||||
Db 65 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECVM 124
|||||

QY 121 KGVSTRVYERA 132
|||||
Db 125 KGVSTRVYERA 136
|||||

RESULT 7

US-09-760-469-917
; Sequence 917, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254
; CURRENT APPLICATION NUMBER: US/09/760,469
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 917
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-469-917

Query Match 100.0%; Score 675; DB 21; Length 136;
Best Local Similarity 100.0%; Pred. No. 2.2e-67;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
|||||
Db 5 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 64
|||||

QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECVM 120
|||||

Db 65 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECVM 124
|||||
QY 121 KGVSTRVYERA 132
|||||
Db 125 KGVSTRVYERA 136
|||||

RESULT 8

US-09-760-469-1429
; Sequence 1429, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254
; CURRENT APPLICATION NUMBER: US/09/760,469
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1429
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-469-1429

Query Match 100.0%; Score 675; DB 21; Length 136;
Best Local Similarity 100.0%; Pred. No. 2.2e-67;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
|||||
Db 5 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 64
|||||

QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECVM 120
|||||
Db 65 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECVM 124
|||||

QY 121 KGVSTRVYERA 132
|||||
Db 125 KGVSTRVYERA 136
|||||

RESULT 9

US-09-760-469-1432
; Sequence 1432, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254
; CURRENT APPLICATION NUMBER: US/09/760,469
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1432
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-469-1432

Query Match 100.0%; Score 675; DB 21; Length 136;
Best Local Similarity 100.0%; Pred. No. 2.2e-67;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
|||||
Db 5 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 64
|||||

QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECVM 120
|||||
Db 65 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECVM 124
|||||

QY 121 KGVSTRVYERA 132
| | | | | | | | | |
Db 125 KGVSTRVYERA 136

RESULT 10

US-09-760-469-1433
; Sequence 1433, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ54
; CURRENT APPLICATION NUMBER: US/09/760,469
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1433
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-469-1433

Query Match 100.0%; Score 675; DB 21; Length 136;
Best Local Similarity 100.0%; Pred. No. 2.2e-67; Indels 0; Gaps 0;
Matches 132; Conservative 0; Mismatches 0;

QY 1 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
| | | | | | | | | |
Db 5 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 64
QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
| | | | | | | | | |
Db 65 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 124
QY 121 KGVSTRVYERA 132
| | | | | | | | | |
Db 125 KGVSTRVYERA 136

RESULT 11

US-09-760-469-1434
; Sequence 1434, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ54
; CURRENT APPLICATION NUMBER: US/09/760,469
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1434
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-469-1434

Query Match 100.0%; Score 675; DB 21; Length 136;
Best Local Similarity 100.0%; Pred. No. 2.2e-67; Indels 0; Gaps 0;
Matches 132; Conservative 0; Mismatches 0;

QY 1 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
| | | | | | | | | |
Db 5 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 64
QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
| | | | | | | | | |
Db 65 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 124

QY 121 KGVSTRVYERA 132
| | | | | | | | | |
Db 125 KGVSTRVYERA 136

RESULT 12

US-09-834-366-17169
; Sequence 17169, Application US/09834366
; GENERAL INFORMATION:
; APPLICANT: Bejani, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.US2.REG
; CURRENT APPLICATION NUMBER: US/09/834,366
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197,873
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 17169
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 62
; OTHER INFORMATION: Xaa = Asp,Glu
; NAME/KEY: UNSURE
; LOCATION: 82
; OTHER INFORMATION: Xaa = Lys,Asn
US-09-834-366-17169

Query Match 96.1%; Score 649; DB 22; Length 129;
Best Local Similarity 98.4%; Pred. No. 1.7e-64;
Matches 127; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
| | | | | | | | | |
Db 1 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
| | | | | | | | | |
Db 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
QY 121 KGVSTRVY 129
| | | | | | | | | |
Db 121 KGVSTRVY 129

RESULT 13

US-09-197-873-17169
; Sequence 17169, Application US/60197873
; GENERAL INFORMATION:
; APPLICANT: Bejani, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.US1.PRO
; CURRENT APPLICATION NUMBER: US/60/197,873
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 17169
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: UNSURE
; LOCATION: 62
; OTHER INFORMATION: Xaa = Asp,Glu
; NAME/KEY: UNSURE
; LOCATION: 82
; OTHER INFORMATION: Xaa = Lys,Asn
US-60-197-873-17169
```

```
Query Match          96.1%; Score 649; DB 24; Length 129;
Best Local Similarity 98.4%; Pred. No. 1.7e-64;
Matches 127; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
    |||||
Db 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
    |||||
Qy 61 TEISFILGOEFDEVTDADRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
    |||||
Db 61 TXISFILGOEFDEVTDADRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
    |||||
Qy 121 KGVTSRVY 129
    |||||
Db 121 KGVTSRVY 129
    |||||
```

```
RESULT 14
US-09-503-596-5
; Sequence 5, Application US/09503596
; GENERAL INFORMATION:
; APPLICANT: Lee et al.
; TITLE OF INVENTION: Inhibiting formation of Artherosclerotic Lesions
; FILE REFERENCE: 21509-042
; CURRENT APPLICATION NUMBER: US/09/503,596
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/119,880
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-503-596-5
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```
Query Match          92.6%; Score 625; DB 19; Length 132;
Best Local Similarity 91.7%; Pred. No. 8.9e-62;
Matches 121; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
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Db 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDLVIRSESTFKN 60
    |||||
Qy 61 TEISFILGOEFDEVTDADRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
    |||||
Db 61 TEISFKLGQEFDEITPDORVKYSITLDGGALVQVQNDGKSTTIKKRRLVDKMLVEECVM 120
    |||||
Qy 121 KGVTSRVYERA 132
    |||||
Db 121 KGVTSRVYERA 132
    |||||
```

```
RESULT 15
US-09-699-146-172
; Sequence 172, Application US/09699146
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka J
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; TITLE OF INVENTION: Compositions Isolated From Bovine Mammary Gland and Methods For Their Use.
```

```
; FILE REFERENCE: 104601
; CURRENT APPLICATION NUMBER: US/09/699,146
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,701
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 262
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 172
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Bovine
US-09-699-146-172
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```
Query Match          84.7%; Score 572; DB 20; Length 132;
Best Local Similarity 83.3%; Pred. No. 8.1e-56;
Matches 110; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
    |||||
Db 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPTLIISLNGGVVITIKSESTFKN 60
    |||||
Qy 61 TEISFILGOEFDEVTDADRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDDKLVEECVM 120
    |||||
Db 61 TEISFKLGQEFDEITPDORVKYSITLDGGALVQVQNDGKSTTIKKRRLVDKMLVEECVM 120
    |||||
Qy 121 KGVTSRVYERA 132
    |||||
Db 121 NGVTATTYERA 132
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Job time: 197 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 24, 2002, 09:14:58 ; Search time 11.74 Seconds
(without alignments)
390.957 Million cell updates/sec

Title: US-09-905-235-1
Perfect score: 675
Sequence: 1 MCDFAFGTGWKLYSSENFDDY.....KLVEECVMKGVTSTRVIERA 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 160442 seqs, 34771459 residues

Total number of hits satisfying chosen parameters: 160442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
- 7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	69.0	133	5	US-09-901-436-7
2	463	68.6	132	5	US-09-901-436-11
3	449	66.5	133	5	US-09-901-436-10
4	445	65.9	132	5	US-09-986-240-2
5	399	59.1	132	5	US-09-971-187-2
6	225	33.3	134	5	US-09-901-436-9
7	212	31.4	135	5	US-09-901-436-8
8	201.5	29.9	138	6	US-10-017-754-328
9	122	18.1	107	5	US-09-901-436-2
10	86	12.7	127	5	US-09-981-353-21
11	74.5	11.0	304	5	US-09-620-394B-4280
12	74.5	11.0	547	5	US-09-708-427-20771
13	74.5	11.0	559	5	US-09-708-427-20770
14	74.5	11.0	610	5	US-09-815-242-13176
15	74.5	11.0	662	5	US-09-708-427-21666
16	69.5	10.3	380	5	US-09-708-427-21665
17	69.5	10.3	446	5	US-09-708-427-21665
18	69.5	10.3	510	5	US-09-708-427-21664
19	69	10.2	380	5	US-09-708-427-35496
20	69	10.2	446	5	US-09-708-427-35495
21	69	10.2	510	5	US-09-979-776-2
22	69	10.2	511	5	US-09-708-427-35494
23	68	10.1	2470	7	US-60-337-358-579
24	67.5	10.0	240	5	US-09-815-242-13453
25	67.5	10.0	241	5	US-09-815-242-13609
26	67.5	10.0	361	5	US-09-708-427-58892

27	67.5	10.0	365	5	US-09-708-427-58891	Sequence 58891, A
28	67.5	10.0	367	5	US-09-708-427-58890	Sequence 58890, A
29	67.5	10.0	602	5	US-09-815-242-10802	Sequence 10802, A
30	67	9.9	237	7	US-60-318-677-20	Sequence 20, Appl
31	67	9.9	339	5	US-09-708-427-15957	Sequence 15957, A
32	67	9.9	342	5	US-09-708-427-15956	Sequence 15956, A
33	67	9.9	399	5	US-09-708-427-15955	Sequence 15955, A
34	65.5	9.7	181	5	US-09-995-493-38	Sequence 38, Appl
35	65.5	9.7	263	5	US-09-708-427-1236	Sequence 1236, Ap
36	65.5	9.7	306	5	US-09-708-427-1235	Sequence 1235, Ap
37	65.5	9.7	357	5	US-09-708-427-1234	Sequence 1234, Ap
38	65.5	9.7	591	5	US-09-815-242-10419	Sequence 10419, A
39	65.5	9.7	856	5	US-09-708-427-15247	Sequence 15247, A
40	65.5	9.7	888	5	US-09-708-427-15246	Sequence 15246, A
41	65.5	9.7	1021	5	US-09-708-427-15245	Sequence 15245, A
42	65	9.6	206	5	US-09-815-242-10335	Sequence 10335, A
43	65	9.6	454	5	US-09-708-427-18105	Sequence 18105, A
44	65	9.6	522	5	US-09-708-427-18104	Sequence 18104, A
45	65	9.6	539	5	US-09-708-427-18103	Sequence 18103, A

ALIGNMENTS

RESULT 1
US-09-901-436-7
Sequence 7, Application US/09901436
GENERAL INFORMATION:
APPLICANT: NI, Jian
Gentz, Reiner
Yu, Guo-Liang
Rosen, Craig A
TITLE OF INVENTION: Cytostatin I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/901,436
FILING DATE: 10-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/361,737
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PF175D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-901-436-7
Query Match 69.0%; Score 466; DB 5; Length 133;
Best Local Similarity 67.9%; Pred. No. 2.6e-38;

Matches 89; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 MDAFVGTWKLVSSENFDYMKYGVGFATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60
 Db 1 MADAFVGTWKLVDKSNFDYMKSLGVGFATRKVASMTKPTTIIIEKNGDTITIKTQSTFKN 60
 QY 61 TEISFILGQEFDEVTAADRKKVKSITTLDDGGVLVHVQKWDGKSTTIKKRREDDKLWVECV 120
 Db 61 TEINFGIIEFEDEVTAADRKKVKSITLDDGGKLIVHVKWNGQETTLTRELVDGKLILTLTH 120
 QY 121 KGVSTRYIER 131
 Db 121 GSVSTRYIER 131

RESULT 2

US-09-901-436-11

; Sequence 11, Application US/09901436

; GENERAL INFORMATION:

; APPLICANT: Ni, Jian

; Gentz, Reiner

; Yu, Guo-Liang

; Rosen, Craig A

; TITLE OF INVENTION: Cytostatin I

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVENUE

; CITY: ROCKVILLE

; STATE: MARYLAND

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/901,436

; FILING DATE: 10-Jul-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/361,737

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: P-43,975

; REFERENCE/DOCKET NUMBER: PF175D2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-610-5772

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 132 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-901-436-11

Query Match 68.6%; Score 463; DB 5; Length 132;

Best Local Similarity 67.2%; Pred. No. 5e-38;

Matches 88; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 1 MDAFVGTWKLVSSENFDYMKYGVGFATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60
 Db 1 MSNFGTWKLVSSENFDYMKALGVGATRLKGLMARTVLIISKGGDIITIRTESTFKN 60

QY 61 TEISFILGQEFDEVTAADRKKVKSITTLDDGGVLVHVQKWDGKSTTIKKRREDDKLWVECV 120
 Db 61 TEISFKLGQEFEEETADNRKTSITVLQKSLNQVQKWDGKSTTIKKRVLNGKVAECKM 120

QY 121 KGVSTRYIER 131
 Db 121 KGVCTRRIYER 131

RESULT 3

US-09-901-436-10

; Sequence 10, Application US/09901436

; GENERAL INFORMATION:

; APPLICANT: Ni, Jian

; Gentz, Reiner

; Yu, Guo-Liang

; Rosen, Craig A

; TITLE OF INVENTION: Cytostatin I

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVENUE

; CITY: ROCKVILLE

; STATE: MARYLAND

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/901,436

; FILING DATE: 10-Jul-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/361,737

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: P-43,975

; REFERENCE/DOCKET NUMBER: PF175D2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-610-5772

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 133 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-901-436-10

Query Match 66.5%; Score 449; DB 5; Length 133;

Best Local Similarity 64.9%; Pred. No. 1.2e-36;

Matches 85; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

QY 1 MDAFVGTWKLVSSENFDYMKYGVGFATRKVAGMAKPNMIIISVNGDVITIKSESTFKN 60
 Db 1 MVDAGLTWKLVDKSNFDYMKSLGVGFATRKQVASMTKPTTIIIEKNGDILTKTHSTFKN 60

QY 61 TEISFILGQEFDEVTAADRKKVKSITTLDDGGVLVHVQKWDGKSTTIKKRREDDKLWVECV 120
 Db 61 TEISFKLGVEFEDEVTAADRKKVKSITLDDGGKLIVHVKWDGQETTLVRELIDGKLILTLTH 120

QY 121 KGVSTRYIER 131
 Db 121 GTAVCTRRIYER 131

RESULT 4

US-09-986-240-2

; Sequence 2, Application US/09986240

GENERAL INFORMATION:
APPLICANT: Weigelt, Johan
APPLICANT: Wikström, Mats
TITLE OF INVENTION: NEW NUCLEAR MAGNETIC RESONANCE SCREENING
FILE REFERENCE: 13425-047001
CURRENT APPLICATION NUMBER: US/09/986,240
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 60/243,626
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: SE 0003811-7
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-09-986-240-2

Query Match 65.9%; Score 445; DB 5; Length 132;
Best Local Similarity 65.1%; Pred. No. 2.8e-36;
Matches 84; Conservative 16; Mismatches 29; Indels 0; Gaps 0;
QY 3 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 62
Db 2 DAFGLTGWKLVDKSNFDDYMKSLVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 61
QY 63 ISFILGQEFDEVTADRRKVKSTITLDGGVLVHVQKWDGKSTIKRKREDDKLVVECVMGK 122
Db 62 ISFKLGVFEFDETTADRRKVKSTITLDGGVLVHVQKWDGQETTLVRELIDGKLTLTLTHGT 121
QY 123 VTSTRVYER 131
Db 122 AVCRTTYEK 130

RESULT 5
US-09-971-187-2
Sequence 2, Application US/09971187
GENERAL INFORMATION:
APPLICANT: Jian Ni et al.
TITLE OF INVENTION: Cytostatin II
FILE REFERENCE: PF221D1
CURRENT APPLICATION NUMBER: US/09/971,187
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/043,646
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: PCT/US95/12540
PRIOR FILING DATE: 1995-09-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 132
TYPE: PRT
ORGANISM: human
US-09-971-187-2

Query Match 59.1%; Score 399; DB 5; Length 132;
Best Local Similarity 56.8%; Pred. No. 8.1e-32;
Matches 75; Conservative 21; Mismatches 36; Indels 0; Gaps 0;
QY 1 MDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
Db 1 MVEAFCAFWKLTSQNFDETKALGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
QY 61 TEISFILGQEFDEVTADRRKVKSTITLDGGVLVHVQKWDGKSTIKRKREDDKLVVECVMG 120
Db 61 TEISFOLGEEFDETTADRRCKSVSLDGLKVLHIQKWDGKSTIKRKREDDKLVVECVMG 120
QY 121 KGVSTRVYERA 132

Db 121 GDVAVRHYEKA 132
RESULT 6
US-09-901-436-9
Sequence 9, Application US/09901436
GENERAL INFORMATION:
APPLICANT: Ni, Jian
Gentz, Reiner
Yu, Guo-Liang
Rosen, Craig A
TITLE OF INVENTION: Cytostatin I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/901,436
FILING DATE: 10-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/361,737
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PF175D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-901-436-9

Query Match 33.3%; Score 225; DB 5; Length 134;
Best Local Similarity 38.6%; Pred. No. 6.3e-15;
Matches 49; Conservative 27; Mismatches 49; Indels 2; Gaps 1;
QY 7 GTWKLVSSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTEISFI 66
Db 7 GTWEMESSENFEGYMKALDIDFATPKIAVRLTQTQKVIDQDGNFKTKTSTFRNYDVDF 66
QY 67 LGQEFDEVT--ADRRKVKSTITLDGGVLVHVQKWDGKSTIKRKREDDKLVVECVMGV 124
Db 67 VGVFEFDEYKSLDNRHVKALVTWEGDLVLCVQKGEKNGKOWIEGDKLYLELTGQDV 126
QY 125 STRVYER 131
Db 127 CROVFKK 133
RESULT 7
US-09-901-436-8
Sequence 8, Application US/09901436
GENERAL INFORMATION:
APPLICANT: Ni, Jian

Genzt, Reiner
Yu, Guo-Liang
Rosen, Craig A
TITLE OF INVENTION: Cytostatin I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/901,436
FILING DATE: 10-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/361,737
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PFI75D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Query Match 31.4%; Score 212; DB 5; Length 135;
Best Local Similarity 35.7%; Pred. No. 1.2e-13;
Matches 46; Conservative 34; Mismatches 47; Indels 2; Gaps 1;
QY 5 FVGWKLVSSENFDDYMKVGVGFATRK--VAGMAKPNMIIISVNGDVITIKSESTFKNTEIS 64
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 5 FTGYKMLVNEFPEYLALDYNVALRKIANLLKPKDEIVQGDHMIIRTLSTFRNYMD 64
QY 65 FILQGEFDE--VTADRRKVKSTITLDGGVLVHVOKWDGKSTTIKRRDDDKLVVECVNKG 122
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 65 FQVGKEFEEDLTGIDRRKMTTWSWDGKLQCVQKGEKGRGTQWIEGDELHLEMRVEG 124
QY 123 VTSTRVYER 131
Db 125 VVCKQVFKK 133

RESULT 8
US-10-017-754-328
; Sequence 328, Application US/10017754
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.

APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.478C18
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 328
LENGTH: 138
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-754-328

Query Match 29.9%; Score 201.5; DB 6; Length 138;
Best Local Similarity 32.4%; Pred. No. 1.3e-12;
Matches 47; Conservative 23; Mismatches 46; Indels 29; Gaps 3;
QY 5 FVGWKLVSSENFDDYMKVGVGFATRK--VAGMAKPNMIIISVNGDVITIKSESTFKNTE 62
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 4 FSGNWKIIRSENFEEELKVLGVNMLRKIAVAASKPAVEIKQEGDFYIKTSTTVTFTE 63
QY 63 ISFILQGEFDEVTADRRKVKSTITLDGGVLVHVOKWDG-----KSTTIK 106
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 64 INFKVGEEPEEQTVDRPKCSLV-----KWSEKNKVVCEQKLLKGEGPKTSWTR 112
QY 107 RKREDDKLVVECVNKGVTSTRVYER 131
Db 113 ELTNDGELILTMTADDVYCTRVYVR 137

RESULT 9
US-09-901-436-2
; Sequence 2, Application US/09901436
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; Yu, Guo-Liang
; Rosen, Craig A
TITLE OF INVENTION: Cytostatin I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/901,436
FILING DATE: 10-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/361,737
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PFI75D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-901-436-2

Query Match 18.1%; Score 122; DB 5; Length 107;
Best Local Similarity 33.8%; Pred. No. 4.7e-05;
Matches 23; Conservative 20; Mismatches 25; Indels 0; Gaps 0;
QY 7 GTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSETFKNTFISFI 66
Db 7 GYRFVSQKNMEDYIQLALNISLAVRKIALLLKPKDEIHQGNHMTVRTLSIFRNTYLFQD 66
QY 67 LGOEFDEV 74
Db 67 VGVKGEV 74

RESULT 10
US-09-981-353-21
; Sequence 21, Application US/09981353
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 21
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 1282225CD1
US-09-981-353-21

Query Match 12.7%; Score 86; DB 5; Length 127;
Best Local Similarity 26.0%; Pred. No. 0.18;
Matches 26; Conservative 17; Mismatches 29; Indels 28; Gaps 3;
QY 4 AFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDV----- 49
Db 2 SFSGYLOLQSOENFEAFMKAIGL-----PEELIQKGRDKGVSEIVQNGKHF 49
QY 50 ITIKSETFKNTFISFILGOEFDEVTDADRKVKSTITLDG 89
Db 50 FTITAGS--KVIONFTVGECELETMTGKVTVVQLEG 87

RESULT 11
US-09-620-394B-4280
; Sequence 4280, Application US/09620394B
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-1067P
; CURRENT APPLICATION NUMBER: US/09/620,394B
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9131
; SEQ ID NO 4280
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..304
; OTHER INFORMATION: xaa is any amino acid

NAME/KEY: misc.feature
LOCATION: 1..304
OTHER INFORMATION: Ceres Seq. ID 1388881
US-09-620-394B-4280

Query Match 11.0%; Score 74.5; DB 5; Length 304;
Best Local Similarity 25.0%; Pred. No. 7.3;
Matches 36; Conservative 19; Mismatches 54; Indels 35; Gaps 6;
QY 3 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKS----- 54
Db 152 EAFSGCGTIVSCKVATDHMGQSRGYGVQFDTDSAK-NAIEKLNGKVLNDKQIFVGPFL 210
QY 55 -----ESTFKNTEISFILGOEFDEVTDADRKVKSTITLDGV--LVHVQKWDGKS----- 102
Db 211 RKEERESAADKMKFTNVYVKNLSEATD--ELKTTFGQYGSISSAVVMRDGDKSRFCGF 269
QY 103 -----TTIKRKREDDK 113
Db 270 VNFENPEDAARAVEALNGKKFDDK 293

RESULT 12
US-09-708-427-20771
; Sequence 20771, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20771
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..547
; OTHER INFORMATION: xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: 1..547
; OTHER INFORMATION: Ceres Seq. ID 1838598
US-09-708-427-20771

Query Match 11.0%; Score 74.5; DB 5; Length 547;
Best Local Similarity 25.0%; Pred. No. 16;
Matches 36; Conservative 19; Mismatches 54; Indels 35; Gaps 6;
QY 3 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKS----- 54
Db 37 EAFSGCGTIVSCKVATDHMGQSRGYGVQFDTDSAK-NAIEKLNGKVLNDKQIFVGPFL 95
QY 55 -----ESTFKNTEISFILGOEFDEVTDADRKVKSTITLDGV--LVHVQKWDGKS----- 102
Db 96 RKEERESAADKMKFTNVYVKNLSEATD--ELKTTFGQYGSISSAVVMRDGDKSRFCGF 154
QY 103 -----TTIKRKREDDK 113
Db 155 VNFENPEDAARAVEALNGKKFDDK 178

RESULT 13
US-09-708-427-20770
; Sequence 20770, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
; TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20770
LENGTH: 559
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..559
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..559
OTHER INFORMATION: Ceres Seq. ID 1838597
US-09-708-427-20770

Query Match 11.0% Score 74.5; DB 5; Length 559;
Best Local Similarity 25.0%; Pred. No. 16;
Matches 36; Conservative 19; Mismatches 54; Indels 35; Gaps 6;
QY 3 DAFVGTWKLVSSNFDDYM-KEVGVGFATRKVAGMAKPNMIISVNGDVITIKS-----54
Db 49 EAFSGCGTIVSCKVATDHMGQSRGYGVQFDTDSAK-NAIEKLNKGVLDNDKQIFVGPFL 107
QY 55 -----ESTFKNTEISFILGQEFDEVTADDRKVKSTIITLDGV--LVHVQKWDGKS-----102
Db 108 RKEERSAADKMKFTNVYVKNLSEATDD-ELKTTFGQYGSISSAVVYMRDGDGKRCFGF 166
QY 103 -----TTIKRKREDDK 113
Db 167 VNFENPEDAARAVEALNGKKFDDK 190

RESULT 14
US-09-815-242-13176
Sequence 13176, Application US/09815242
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
TITLE OF INVENTION: ELITRA 011A
FILE REFERENCE: ELITRA 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13176
LENGTH: 610
TYPE: PRT
ORGANISM: Streptococcus pneumoniae

US-09-815-242-13176

Query Match 11.0% Score 74.5; DB 5; Length 610;
Best Local Similarity 30.3%; Pred. No. 18;
Matches 27; Conservative 15; Mismatches 40; Indels 7; Gaps 3;
QY 21 MKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSEST-----FKNTEISFILGQEFDEVT 76
Db 447 MQKVHAGLAVD--TGVEKDNIIFMSNGDVIALTADSARIAGHFNAQDIYVDGNRIGEIGA 504
QY 77 DDRKVKSTIITLDGVLVHVQKWDGKSTTI 105
Db 505 AVLKDRDLSEDSGVVLA-VATVDFKSQMI 532

RESULT 15
US-09-708-427-20769
Sequence 20769, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20769
LENGTH: 662
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..662
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..662
OTHER INFORMATION: Ceres Seq. ID 1838596
US-09-708-427-20769

Query Match 11.0% Score 74.5; DB 5; Length 662;
Best Local Similarity 25.0%; Pred. No. 20;
Matches 36; Conservative 19; Mismatches 54; Indels 35; Gaps 6;
QY 3 DAFVGTWKLVSSNFDDYM-KEVGVGFATRKVAGMAKPNMIISVNGDVITIKS-----54
Db 152 EAFSGCGTIVSCKVATDHMGQSRGYGVQFDTDSAK-NAIEKLNKGVLDNDKQIFVGPFL 210
QY 55 -----ESTFKNTEISFILGQEFDEVTADDRKVKSTIITLDGV--LVHVQKWDGKS-----102
Db 211 RKEERSAADKMKFTNVYVKNLSEATDD-ELKTTFGQYGSISSAVVYMRDGDGKRCFGF 269
QY 103 -----TTIKRKREDDK 113
Db 270 VNFENPEDAARAVEALNGKKFDDK 293

Search completed: January 24, 2002, 09:18:03
Job time: 185 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 24, 2002, 09:13:58 ; Search time 14.4 Seconds
(without alignments)
698.267 Million cell updates/sec

Title: US-09-905-235-1
Perfect score: 675
Sequence: 1 MCDFAVGTWKLVSSENFDDY.....KLVVECVMKGVSTRVYERA 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 68.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	675	100.0	132	1 FZHUF	fatty acid-binding
2	623	92.3	132	2 B25952	myelin P2 protein
3	578	85.6	132	2 S57744	adipocyte-type fat
4	486	72.0	132	1 MPR92	myelin P2 protein
5	477	70.7	133	2 A27452	fatty acid-binding
6	466	69.0	133	2 PC4011	fatty acid-binding
7	463	68.6	132	1 MPH02	myelin P2 protein
8	450	66.7	132	2 JH0407	myelin P2 protein
9	449	66.5	133	1 FZHUC	fatty acid-binding
10	448	66.4	131	1 MPB02	myelin P2 protein
11	446	66.1	133	2 A34676	fatty acid-binding
12	425	63.0	131	2 S06479	fatty acid-binding
13	392	58.1	132	2 A49184	fatty acid-binding
14	390	57.8	132	2 I52524	testis lipid bindi
15	385	57.0	132	2 I56510	fatty acid binding
16	381	56.4	132	2 I58161	lipid-binding prot
17	381	56.4	132	2 I48923	fatty acid-binding
18	378	56.0	132	2 S20297	fatty acid-binding
19	366	54.2	135	2 I56326	fatty acid-binding
20	362	53.6	135	2 A47497	lipid-binding prot
21	361	53.5	135	2 JC2201	fatty acid-binding
22	307.5	45.6	135	2 T15205	hypothetical prote
23	300.5	44.5	136	2 T15207	hypothetical prote
24	256.5	38.0	137	2 T25123	hypothetical prote
25	242.5	35.9	133	2 A48578	fatty acid-binding
26	231.5	34.3	134	2 S29600	fatty acid-binding
27	229.5	34.0	133	2 A39818	14K fatty acid-bin
28	227	33.6	133	2 A44870	fatty acid-binding
29	227	33.6	134	2 S34717	retinol-binding pr

30 225 33.3 134 2 A29065 retinol-binding pr
31 223 33.0 134 2 S45378 cellular retinol b
32 223 33.0 134 2 S43470 fatty-acid-binding
33 222 32.9 137 1 R3HU1 retinoic acid-bind
34 220 32.6 137 1 R3BOA retinoic acid-bind
35 220 32.6 137 2 A35825 retinoic acid-bind
36 218 32.3 135 1 R3RTO retinol-binding pr
37 212 31.4 135 1 R3HU0 retinol-binding pr
38 212 31.4 135 2 S16355 retinol-binding pr
39 206 30.5 134 2 S69360 retinol-binding pr
40 203.5 30.1 138 2 A42495 retinoic acid-bind
41 201.5 29.9 138 1 R3HU2 retinoic acid-bind
42 197.5 29.3 138 2 I51265 xCRABP - African c
43 196 29.0 139 2 F53298 cellular retinoic
44 191 28.3 95 2 A61629 retinoic acid-bind
45 190 28.1 132 1 F3HU1 fatty acid-binding

ALIGNMENTS

RESULT 1

FZHUF
fatty acid-binding protein, adipocyte - human
N:Alternate names: adipocyte lipid-binding protein (ALBP); fatty acid binding protein
C:Species: Homo sapiens (man)
C:Date: 20-Dec-1989 #sequence_revision 03-May-1996 #text_change 22-Jun-1999
C:Accession: A33363
R:Baxa, C.A.; Sha, R.S.; Buelte, M.K.; Smith, A.J.; Matarese, V.; Chinander, L.L.; Bou
Biochemistry 28, 8683-8690, 1989
A:Title: Human adipocyte lipid-binding protein: purification of the protein and cloni
A:Reference number: A33363; MUID:90105397
A:Accession: A33363
A:Molecule type: mRNA
A:Residues: 1-132 <BAX>
A:Cross-references: GB:J02874; NID:g178346; PIDN:AAA51689.1; PID:g178347
A:Experimental source: subcutaneous fat
C:Genetics:
A:Gene: GDB:FABP4
A:Cross-references: GDB:128030
A:Map position: lp33-lp32
C:Superfamily: myelin P2 protein
C:Keywords: blocked amino end; lipid binding; phosphoprotein
F:2/Modified site: blocked amino end (Cys) (in mature form) (probably acetylated) #st
F:20/Modified site: phosphate (Tyr) (covalent) #status predicted
F:127,129/Binding site: fatty acid (Arg, Tyr) #status predicted

Query Match 100.0%; Score 675; DB 1; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-54;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCDFAVGTWKLVSSENFDDYMKVEGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60

Db 1 MCDFAVGTWKLVSSENFDDYMKVEGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60

QY 61 TEISFILGQEFDEVTADRRKVKSTITLDGGVLHVQKWDGKSTIKRKREDKLVVECV 120

Db 61 TEISFILGQEFDEVTADRRKVKSTITLDGGVLHVQKWDGKSTIKRKREDKLVVECV 120

QY 121 KGVSTRVYERA 132

Db 121 KGVSTRVYERA 132

RESULT 2

B25952
myelin P2 protein homolog - mouse
N:Alternate names: adipocyte lipid-binding protein; adipocyte P2 protein
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2000
C:Accession: B25952; PC1249; A24884; A05089; I49440; I49467
R:Phillips, M.; Djian, P.; Green, H.

J. Biol. Chem. 251, 10821-10827, 1986
 A:Title: The nucleotide sequence of three genes participating in the adipose differentiation
 A:Reference number: A92553; MUID:86278164
 A:Accession: B25952
 A:Molecule type: DNA
 A:Residues: 1-132 <PHI>
 A:Cross-references: GB:M13385; NID:g198718; PIDN:AAA39417.1; PID:g387401
 A:Note: the authors translated the codon GTG for residue 111 as Gly
 R:Bansal, M.P.; Medina, D.
 Biochem. Biophys. Res. Commun. 191, 61-69, 1993
 A:Title: Expression of fatty acid-binding proteins in the developing mouse mammary gland
 A:Reference number: PC1248; MUID:93191717
 A:Accession: PC1249
 A:Molecule type: protein
 A:Residues: 25-35;37-51;59-88 <BAN>
 A:Experimental source: mammary gland
 R:Hunt, C.R.; Ro, J.H.S.; Dobson, D.E.; Min, H.Y.; Spiegelman, B.M.
 Proc. Natl. Acad. Sci. U.S.A. 83, 3786-3790, 1986
 A:Title: Adipocyte P2 gene: Developmental expression and homology of 5'-flanking sequence
 A:Reference number: A24884; MUID:86233319
 A:Accession: A24884
 A:Molecule type: DNA
 A:Residues: 1-39,'T',41-110,'G',112-132 <HUN>
 A:Cross-references: GB:M13264; NID:g200183; PIDN:AAA39870.1; PID:g387504
 A:Note: the authors translated the codon ACC for residue 40 as Ser
 R:Bernlohr, D.A.; Angus, C.W.; Lane, M.D.; Bolanowski, M.A.; Kelly Jr., T.J.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5468-5472, 1984
 A:Title: Expression of specific mRNAs during adipose differentiation: identification of
 A:Reference number: A05089; MUID:84298159
 A:Accession: A05089
 A:Molecule type: mRNA
 A:Residues: 1-110,'G',112-132 <BER>
 A:Cross-references: GB:K02109; NID:g198716; PIDN:AAA39416.1; PID:g293695
 J. Biol. Chem. 263, 14544-14551, 1988
 A:Title: Purification of murine adipocyte lipid-binding protein. Characterization as a
 A:Reference number: A30810; MUID:89008309
 A:Accession: A30810
 A:Molecule type: protein
 A:Residues: 2-110,'G',112-132 <MAT>
 R:Cook, K.S.; Hunt, C.R.; Spiegelman, B.M.
 J. Cell Biol. 100, 514-520, 1985
 A:Title: Developmentally regulated mRNAs in 3T3-adipocytes: Analysis of transcriptional
 A:Reference number: I49440; MUID:85105214
 A:Accession: I49440
 A:Molecule type: protein
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 11-110,'G',112-132 <RES>
 A:Cross-references: GB:M28726; NID:g191492; PIDN:AAA37112.1; PID:g191493
 R:Cook, J.S.; Lucas, J.J.; Sibley, E.; Bolanowski, M.A.; Christy, R.J.; Kelly, T.J.; Lan
 Proc. Natl. Acad. Sci. U.S.A. 85, 2949-2953, 1988
 A:Title: Expression of the differentiation-induced gene for fatty acid-binding protein
 A:Reference number: I49467; MUID:88203618
 A:Accession: I49467
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-11 <RES>
 A:Cross-references: GB:M20497; NID:g191743; PIDN:AAA37188.1; PID:g191744
 A:Experimental source: 3T3-L1 cells
 C:Genetics:
 A:Introns: 25/1; 82/3; 116/3
 C:Superfamily: myelin P2 protein
 C:Keywords: lipid binding; phosphoprotein
 Query Match 92.3%; Score 623; DB 2; Length 132;
 Best Local Similarity 91.7%; Pred. No. 8.6e-50;
 Matches 121; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIIISVNGDVTIKSESTFKN 60
 Db 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIIISVNGDVTIKSESTFKN 60

Qy 61 TEISFILGQEFDEVTADRRKVKSTITLDGVLVHVQKWDGKSTTIKRRKDDKLWVECV 120
 Db 61 TEISFLGVFEFDEITADRRKVKSIITLDGALVQVQKWDGKSTTIKRRKDDKLWVECV 120
 Qy 121 KGVTSRTRYERA 132
 Db 121 KGVTSRTRYERA 132
 RESULT 3
 S57744
 adipocyte-type fatty acid binding protein - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 13-Aug-1999
 C:Accession: S57744
 R:Specht, B.; Bartetzko, N.; Kuhl, H.; Franke, R.; Boerchers, T.; Spener, F.
 submitted to the EMBL Data Library, June 1995
 A:Description: Mammary derived growth inhibitor - not a distinct protein but a mix of
 A:Reference number: S57744
 A:Accession: S57744
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-132 <SPE>
 A:Cross-references: EMBL:X89244; NID:g895753; PIDN:CAA61532.1; PID:g895754
 C:Superfamily: myelin P2 protein
 Query Match 85.6%; Score 578; DB 2; Length 132;
 Best Local Similarity 84.1%; Pred. No. 1.1e-45;
 Matches 111; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
 Qy 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIIISVNGDVTIKSESTFKN 60
 Db 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIIISVNGDVTIKSESTFKN 60
 Qy 61 TEISFILGQEFDEVTADRRKVKSTITLDGVLVHVQKWDGKSTTIKRRKDDKLWVECV 120
 Db 61 TEISFLGQEFDEITPDPRKVKSVNLDEGALVQVQKWDGKSTTIKRRKDDKLWVECV 120
 Qy 121 KGVTSRTRYERA 132
 Db 121 NGVTATRYERA 132
 RESULT 4
 MPRB2
 myelin P2 protein - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Jun-1980 #sequence_revision 10-May-1996 #text_change 22-Jun-1999
 C:Accession: A28081; A92266; A92372; A03145
 R:Narayanan, V.; Barbosa, E.; Reed, R.; Tennekoon, G.
 J. Biol. Chem. 263, 8332-8337, 1988
 A:Title: Characterization of a cloned cDNA encoding rabbit myelin P-2 protein.
 A:Reference number: A28081; MUID:88228063
 A:Accession: A28081
 A:Molecule type: mRNA
 A:Residues: 1-132 <NAR>
 A:Cross-references: GB:J03744; NID:g165657; PIDN:AAA31451.1; PID:g165658
 A:Note: translation of initiator Met is not shown
 R:Ishaque, A.; Hofmann, T.; Rhee, S.; Eylar, E.H.
 J. Biol. Chem. 255, 1058-1063, 1980
 A:Title: The NH-2-terminal region of the P2 protein from rabbit sciatic nerve myelin.
 A:Reference number: A92266; MUID:80094496
 A:Accession: A92266
 A:Molecule type: protein
 A:Residues: 2-56 <ISI>
 R:Ishaque, A.; Hofmann, T.; Eylar, E.H.
 J. Biol. Chem. 257, 592-595, 1982
 A:Title: The complete amino acid sequence of the rabbit P2 protein.
 A:Reference number: A92372; MUID:82098098
 A:Accession: A92372
 A:Molecule type: protein
 A:Residues: 56-72,'Q',74-83,'T',85-98,'N',100-132 <IS2>

A; Molecule type: protein
A; Accession: A2819/
A; Residues: 2-10; 46-53 <GIB>

expression of fatty acid binding proteins in the developing mouse mammary gland

5 FVGTWKLVSSENFDDYMKVEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTEIS 64 QY

Qy	1	MCDAFVGWTKVLSBENEDDYMKYGVGFGATRKVAGMAKPNIIISVNGDVITIKSBSTFKN	60
Db	1	MYDAFVGWTKVLDSKNFEDYMKSLGVGFATRGVNTKPTTIIENVNGDPTVIIKTOSTFKN	60
Qy	61	TEISFILGQEFDEVTAADRRKVKSTITLLDGGVLHVQKWDGKSTTIKKRREDDKLWVFCVM	12
Db	61	TEISFKLGEVDETTADDRKVKSTVTLDDGKLHVHQKWDGKSTSLVREMGDKLLITLTH	12

QY 121 KGVSTRVYER 131
 DB 121 GTAVCTRYEK 131

RESULT 12
 S06479
 fatty acid-binding protein, brain - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 24-Nov-1999
 C:Accession: S06479; JH0198
 R:Schoentgen, F.; Pignede, G.; Bonanno, L.M.; Jolles, P.
 Eur. J. Biochem. 185, 35-40, 1989
 A:Title: Fatty acid-binding protein from bovine brain. Amino acid sequence and some prop
 A:Reference number: S06479; MUID:90032683
 A:Accession: S06479
 A:Molecule type: protein
 A:Residues: 1-131 <SCH>
 A:Experimental source: brain
 A:Note: 11-Val, 12-Asp, 14-Lys, 18-Asp, 33-Ala, 34-Ser, 40-Thr, 43-Glu, 44-Lys, 49-Val,
 R:Schoentgen, F.; Bonanno, L.M.; Pignede, G.; Jolles, P.
 Mol. Cell. Biochem. 98, 35-39, 1990
 A:Title: Amino acid sequence and some ligand binding properties of fatty acid-binding pr
 A:Reference number: JH0198; MUID:91094811
 A:Contents: annotation
 C:Comment: Synaptosomal Na+-dependent amino acid transport is stimulated by the fatty ac
 C:Superfamily: myelin P2 protein
 C:Keywords: blocked amino end
 F:1/Modified site: blocked amino end (Val) (probably acetylated) #status experimental

Query Match 63.0%; Score 425; DB 2; Length 131;
 Best Local Similarity 62.0%; Pred. No. 8.8e-32;
 Matches 80; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

QY 3 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIIISVNGDVIITIKSESTFKNTE 62
 DB 2 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIIISVNGDVIITIKSESTFKNTE 61
 QY 63 ISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLIVVECVKM 122
 DB 62 ISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLIVVECVKM 121
 QY 123 VTSTRVYER 131
 DB 122 VVAVRHYEK 130

RESULT 13
 A49184
 fatty acid-binding protein - chicken
 N:Alternate names: lipid-binding protein
 C:Species: Gallus gallus (chicken)
 C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
 C:Accession: A49184; S26599
 R:Godbout, R.
 Exp. Eye Res. 56, 95-106, 1993
 A:Title: Identification and characterization of transcripts present at elevated levels i
 A:Reference number: A49184; MUID:93162137
 A:Accession: A49184
 A:Molecule type: mRNA
 A:Residues: 1-132 <GOD>
 A:Cross-references: EMBL:X65459; NID:963230; PIDN:CAA46451.1; PID:g63231
 A:Experimental source: retina
 A:Note: sequence extracted from NCBI backbone (NCBIP:124757)
 C:Superfamily: myelin P2 protein

Query Match 58.1%; Score 392; DB 2; Length 132;
 Best Local Similarity 56.1%; Pred. No. 8.9e-29;
 Matches 74; Conservative 19; Mismatches 39; Indels 0; Gaps 0;

QY 1 MCDAPVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIIISVNGDVIITIKSESTFKN 60
 DB 1 MVEAFCAWKALADSHNFDYMKVGVGFATRKVAGMAKPNMIIISVNGDVIITIKSESTFKN 60

QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLIVVECVM 120
 DB 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLIVVECVM 120

QY 121 KGVSTRVYER 132
 DB 121 GDVVAVRHYEK 132

RESULT 14
 I52524
 testis lipid binding protein - rat
 N:Alternate names: 15 kDa perforatorial protein PERF 15
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 13-Aug-1999
 C:Accession: I52524; I53089
 R:Schmitt, M.C.; Jamison, R.S.; Orgebin-Crist, M.C.; Ong, D.E.
 Biol. Reprod. 51, 239-245, 1994
 A:Title: A novel, testis-specific member of the cellular lipophilic transport protein
 A:Reference number: I52524; MUID:95035569
 A:Accession: I52524
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-132 <RES>
 A:Cross-references: EMBL:U07870; NID:9469051; PIDN:AAA68627.1; PID:g469052
 R:Oko, R.J.; Morales, C.C.; Oki, R.; Morales, C.R.
 Dev. Biol. 166, 235-245, 1994
 A:Title: A novel testicular protein, with sequence similarities to a family of lipid
 A:Reference number: I53089; MUID:95046905
 A:Accession: I53089
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-132 <RES2>
 A:Cross-references: EMBL:U09022; NID:g538268; PIDN:AAA67873.1; PID:g538269
 C:Superfamily: myelin P2 protein

Query Match 57.8%; Score 390; DB 2; Length 132;
 Best Local Similarity 56.5%; Pred. No. 1.4e-28;
 Matches 74; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 1 MCDAPVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIIISVNGDVIITIKSESTFKN 60
 DB 1 MIEPFLGTWKLVSSENFENYRELVECEPRKACLIKPSVISFNGERMIDQAGSACRN 60

QY 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLIVVECVM 120
 DB 61 TEISFILGQEFDEVTADDRKVKSLITFEGGSMIQIQLRWLQKQTIKKRIVDGRWVECTM 120

QY 121 KGVSTRVYER 131
 DB 121 NNVTSTRYER 131

RESULT 15
 I56510
 fatty acid binding protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999
 C:Accession: I56510
 R:Bennett, E.; Stenvers, K.L.; Lund, P.K.; Popko, B.
 J. Neurochem. 63, 1616-1624, 1994
 A:Title: Cloning and characterization of a cDNA encoding a novel fatty acid binding p
 A:Reference number: I56510; MUID:95016702
 A:Accession: I56510
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-132 <RES>

A:Cross-references: EMBL:U02096; NID:g476081; PIDN:AAA60455.1; PID:g476082
C:Superfamily: myelin P2 protein

Query Match	57.0%;	Score 385;	DB 2;	Length 132;
Best Local Similarity	55.3%;	Pred. No. 3.9e-28;		
Matches	73;	Conservative 19;	Mismatches 40;	Indels 0; Gaps 0;

Qy	1	MCDAFVGTWKLVSSENFDDYKKEVGVGFPATRKVAGMAKPNMIIISVNGDVITIKSESTFKN	60
Db	1	MVDAFCATWKLTDSONFDEYKALGVGFATRGVGNVTKPTVIISQEGGKWIQTCTFKN	60
Qy	61	TEISFILGGEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKREDDKLVECVN	120
Db	61	TEISFQLGEEFEETSIDDRNCKSVIRLDGDKLIHVQKWDGKTCVREIKDGKVVVTLTF	120
Qy	121	KGVTSTRVYERA	132
Db	121	GDVVAVRCYEKA	132

Search completed: January 24, 2002, 09:16:01
Job time: 123 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 24, 2002, 09:15:23 ; Search time 11.7 Seconds
(without alignments)
413.654 Million cell updates/sec

Title: US-09-905-235-1

Perfect score: 675

Sequence: 1 MCDFAVGTWKLVSSENFDDY.....KLVVECVKGVSTRYERA 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	670	99.3	131	1 FABA_HUMAN	P15090 homo sapien
2	620	91.9	131	1 FABA_MOUSE	P04117 mus musculu
3	608	90.1	131	1 FABA_PIG	Q97788 sus scrofa
4	607	89.9	131	1 FABA_RAT	P70623 rattus norv
5	573	84.9	131	1 FABA_BOVIN	P48035 bos taurus
6	482	71.4	131	1 MYP2_RABIT	P02691 oryctolagus
7	472	69.9	132	1 FABH_RAT	P07483 rattus norv
8	466	69.0	132	1 FABH_MOUSE	P11404 mus musculu
9	459	68.0	131	1 MYP2_HUMAN	P02689 homo sapien
10	448	66.4	131	1 MYP2_BOVIN	P02690 bos taurus
11	446	66.1	131	1 MYP2_MOUSE	P24526 mus musculu
12	445	65.9	132	1 FABH_HUMAN	P05413 homo sapien
13	442	65.5	132	1 FABH_BOVIN	P10790 bos taurus
14	442	65.5	132	1 FABH_PIG	Q02772 sus scrofa
15	425	63.0	131	1 FABB_BOVIN	Q09139 bos taurus
16	424	62.8	132	1 FABB_ONCMY	O13008 oncorhynch
17	395	58.5	131	1 FABB_HUMAN	O15540 homo sapien
18	390	57.8	132	1 TLBP_RAT	P55054 rattus norv
19	388	57.5	131	1 FABB_CHICK	Q05423 gallus gall
20	386	57.2	132	1 TLBP_MOUSE	Q08716 mus musculu
21	381	56.4	131	1 FABB_RAT	P55051 rattus norv
22	378	56.0	132	1 FABL_GINGI	P80049 ginglymosto
23	377	55.9	131	1 FABB_MOUSE	P51880 mus musculu
24	367	54.4	135	1 FABB_BOVIN	P55052 bos taurus
25	366	54.2	135	1 FABB_HUMAN	Q01469 homo sapien
26	362	53.6	135	1 FABB_MOUSE	Q05816 mus musculu
27	361	53.5	135	1 FABB_RAT	P55053 rattus norv
28	326	48.3	114	1 FABL_LAMJA	P82188 lampetra ja
29	270.5	40.1	133	1 FABB_ECHGR	Q02970 echinococcu
30	250	37.0	131	1 FABB_LEPDS	Q9u5p1 lepidoglyph
31	238	35.3	130	1 FABB_BLOTA	Q17284 blomia trop
32	229.5	34.0	133	1 FABB_SCHMA	P29498 schistosoma
33	227	33.6	133	1 FABB_SCHGR	P41496 schistocerc

34	227	33.6	133	1 RET2_MOUSE	Q08652 mus musculu
35	225	33.3	133	1 RET2_HUMAN	P50120 homo sapien
36	225	33.3	133	1 RET2_RAT	P06768 rattus norv
37	223	33.0	133	1 RET2_PIG	P50121 sus scrofa
38	222	32.9	136	1 RET3_HUMAN	P29762 homo sapien
39	221	32.7	133	1 FABM_LOCM1	P41509 locusta mig
40	220	32.6	136	1 RET3_BOVIN	P02695 bos taurus
41	218	32.3	134	1 RET1_RAT	P02696 rattus norv
42	215	31.9	136	1 RET3_FUGRU	O42386 fugu rubrip
43	212	31.4	134	1 RET1_HUMAN	P09455 homo sapien
44	212	31.4	134	1 RET1_MOUSE	Q00915 mus musculu
45	206.5	30.6	137	1 RET4_MOUSE	P22935 mus musculu

ALIGNMENTS

RESULT 1

FABA_HUMAN

ID FABA_HUMAN STANDARD; PRT; 131 AA.

AC P15090;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE FATTY ACID-BINDING PROTEIN, ADIPOCYTE (AFABP) (ADIPOCYTE LIPID-BINDING

DE PROTEIN) (ALBP) (A-FABP).

GN FAPB4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90105397; PubMed=2481498;

RA Baxa C.A., Sha R.S., Buel M.K., Smith A.J., Matarese V.,

RA Chinander L.L., Boundy K.L., Bernlohr D.A.;

RT "Human adipocyte lipid-binding protein: purification of the protein

RT and cloning of its complementary DNA.";

RL Biochemistry 28:8683-8690(1989)

CC -1- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG

CC CHAIN FATTY ACID AND RETINOIC ACID.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).

CC -1- SIMILARITY: BELONGS TO THE FAPB/P2/CRBP/CRABP FAMILY OF

CC TRANSPORTERS.

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CC EMBL; J02874; AA51689.1; ..

DR PIR; A33363; A33363.

DR HSSP; P04117; LALB.

DR MIM; 600434; ..

DR InterPro; IPR000463; Fatty_acid_BP.

DR InterPro; IPR000566; Lipoclin_cycFABP.

DR Pfam; PF00061; Lipocalin; 1.

DR PRINTS; PR00178; FATTYACIDBP.

DR PROSITE; PS00214; FAPB; 1.

DR Transport; Lipid-binding; Phosphorylation.

FT INIT_MET 0 0 BY SIMILARITY.

FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)

FT (BY SIMILARITY).

SQ SEQUENCE 131 AA; 14588 MW; 81C241B63DD98235 CRC64;

Query Match

Best Local Similarity 99.3%; Score 670; DB 1; Length 131;

Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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FT STRAND 59 64
FT TURN 66 67
FT STRAND 70 73
FT TURN 75 76
FT STRAND 79 87
FT TURN 88 89
FT STRAND 90 97
FT TURN 98 99
FT STRAND 100 109
FT TURN 110 111
FT STRAND 112 119
FT TURN 120 121
FT STRAND 122 130
SQ SEQUENCE 131 AA; 14519 MW; ED57D4E2774B8E32 CRC64;

Query Match 91.9%; Score 620; DB 1; Length 131;
Best Local Similarity 91.6%; Pred. No. 7.2e-49;
Matches 120; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 CDAFVGWTKLVSSNFDDYMKVGVGFATRKVAGMKNPMIISVNGDVITIKSESTFKNT 61
DB 1 CDAFVGWTKLVSSNFDDYMKVGVGFATRKVAGMKNPMIISVNGDLVITIRSESTFKNT 60

QY 62 EISFILGOEFDEVTDADRKVKSTITLDGGVLHVQKWDGKSTTIKRREDDKLVVECVMK 121
DB 61 EISFKLGVGEDEVTDADRKVKSTITLDGGALVQVQKWDGKSTTIKRKRDGDKLVVECVMK 120

QY 122 GVTSTRYVERA 132
DB 121 GVTSTRYVERA 131

RESULT 3
FABA_PIG
ID FABA_PIG STANDARD; PRT; 131 AA.
AC Q97788;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FATTY ACID-BINDING PROTEIN, ADIPOCYTE (AFABP) (ADIPOCYTE LIPID-BINDING
DE PROTEIN) (ALBP) (A-FABP) (AP2).
GN FABP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=DUCOC; TISSUE=Liver;
RX MEDLINE=9099248; PubMed=9880671;
RA Gerbens F., Jansen A., van Erp A.J.M., Harders F., Meuwissen T.H.E.,
RA Rettenberger G.F.W., Veerkamp J.H., te Pas M.F.W.;
RT "The adipocyte fatty acid-binding protein locus: characterization and
RT association with intramuscular fat content in pigs.";
RL Mamm. Genome 9:1022-1026(1998).
RN [2]
RP SEQUENCE OF 36-47, AND TISSUE SPECIFICITY.
RC TISSUE=Fat;
RX MEDLINE=90241143; PubMed=2334399;
RA Armstrong M.K., Bernlohr D.A., Storch J., Clarke S.D.;
RA "The purification and characterization of a fatty acid binding protein
RT specific to pig (Sus domesticus) adipose tissue.";
RL Biochem. J. 267:373-378(1990).
CC -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID.
CC -!- FUNCTION: INVOLVED IN THE REGULATION OF INTRAMUSCULAR FAT
CC ACCRETION.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -!- TISSUE SPECIFICITY: ADIPOSE TISSUE.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTER.
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CC -----
CC EMBL; Y16039; CAA75995.1; -
CC HSSP; P04117; ILID
CC InterPro; IPR000463; Fatty_acid_BP.
CC InterPro; IPR000566; Lipoclin_cytrFABP.
CC Pfam; PF00061; lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
CC Transport; Lipid-binding; Phosphorylation.
CC INIT_MET 0
CC MOD_RES 19 19
CC PHOSPHORYLATION (BY TYR-KINASES)
CC (BY SIMILARITY).
CC SEQUENCE 131 AA; 14545 MW; 656CB0CA08CD4AB2 CRC64;

Query Match 90.1%; Score 608; DB 1; Length 131;
Best Local Similarity 88.5%; Pred. No. 8.4e-48;
Matches 116; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 2 CDAFVGWTKLVSSNFDDYMKVGVGFATRKVAGMKNPMIISVNGDVITIKSESTFKNT 61
DB 1 CDAFVGWTKLVSSNFDDYMKVGVGFATRKVAGMKNPMIITVNGDMITIRSESTFKNT 60

QY 62 EISFILGOEFDEVTDADRKVKSTITLDGGVLHVQKWDGKSTTIKRREDDKLVVECVMK 121
DB 61 EIAFKLGQEFDEVTDADRKVKSTITLDGGALVQVQKWDGKSTTIKRKIVDDKLVVECVMK 120

QY 122 GVTSTRYVERA 132
DB 121 GVTATRIYERA 131

RESULT 4
FABA_RAT
ID FABA_RAT STANDARD; PRT; 131 AA.
AC P70623;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FATTY ACID-BINDING PROTEIN, ADIPOCYTE (AFABP) (ADIPOCYTE LIPID-BINDING
DE PROTEIN) (ALBP).
GN FABP4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Prinsen C., Veerkamp J.H.;
RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC CHAIN FATTY ACID AND RETINOIC ACID.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
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CC -----
CC EMBL; U75581; AAB18344.1; -
CC
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CC -----
DR EMBL; J03744; AAA31451.1;
DR PIR; A03145; MPRB2.
DR PIR; A28081; A28081.
DR HSP; P02690; 1PMP.
DR InterPro; IPR000463; Fatty_acid_BP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FAPB; 1.
KW Myelin; Lipid-binding; Transport; Acetylation.
FT INIT_MET 0
FT MOD_RES 1
FT CONFLICT 72 72 E -> Q (IN REF. 3).
FT CONFLICT 83 83 I -> T (IN REF. 3).
FT CONFLICT 98 98 D -> N (IN REF. 3).
SQ SEQUENCE 131 AA; 14791 MW; E53788F693BC6A0E CRC64;
Query Match 71.4%; Score 482; DB 1; Length 131;
Best Local Similarity 72.4%; Pred. No. 1.5e-36;
Matches 92; Conservative 14; Mismatches 21; Indels 0; Gaps 0;
QY 5 FVGTWKLVSSENFDDYMKVGVGFATRKVAGNAKPNMIIISVNGVDVITIKSESTFKNTEIS 64
DB 4 FVGTWKLVSSENFDDYMKALGVGLATRLGNLAKPNVSIKSKGDIITITESTFKNTEIS 63
QY 65 FILGQFEDEVTDADKRVKSTITLDGVLVHVQKWDGKSTTIKKRREDDKLVVCEYKMGVT 124
DB 64 PKLGQFEETADNKRKTSITLREGALNQVQKWDGKETTIRKLKLVQDKWVVECKMGVV 123
QY 125 STRVYER 131
DB 124 CTRIYEK 130
RESULT 7
FAPB_RAT 7
ID FAPB_RAT STANDARD; PRT; 132 AA.
DT 01-APR-1988 (Rel. 07, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FATTY ACID-BINDING PROTEIN, HEART (H-FAPB).
CN FAPB3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87250640; PubMed=3036869;
RA Heckerroth R.O., Birkenmeier E.H., Levin M.S., Gordon J.I.;
RT "Analysis of the tissue-specific expression, developmental
RT regulation, and linkage relationships of a rodent gene encoding heart
RT fatty acid binding protein.";
RL J. Biol. Chem. 262:9709-9717(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88107756; PubMed=3427112;
RA Claffey K.P., Herrera V.L., Brecher P., Ruiz-Opazo N.;
RT "Cloning and tissue distribution of rat heart fatty acid binding
RT protein mRNA: identical forms in heart and skeletal muscle.";
RL Biochemistry 26:7900-7904(1987).
RN [3]
RP SEQUENCE.
RX MEDLINE=88153733; PubMed=3162235;
RA Gibson B.W., Yu Z., Aberth W., Burlingame A.L., Bass N.M.;
RT "Revision of the blocked N terminus of rat heart fatty acid-binding
RT protein by liquid secondary ion mass spectrometry.";
RL J. Biol. Chem. 263:4182-4185(1988).
RN [4]

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RP PRELIMINARY SEQUENCE.
RX MEDLINE=86250713; PubMed=2424895;
RA Sacchetti J.C., Said B., Schulz H., Gordon J.I.;
RT "Rat heart fatty acid-binding protein is highly homologous to the
RT murine adipocyte 422 protein and the P2 protein of peripheral nerve
RT myelin.";
RL J. Biol. Chem. 261:8218-8223(1986).
RN [5]
RP SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=91170283; PubMed=2005132;
RA Kimura H., Odani S., Nishi S.-I., Sato H., Arakawa M., Ono T.;
RT "Primary structure and cellular distribution of two fatty
RT acid-binding proteins in adult rat kidneys.";
RL J. Biol. Chem. 266:5963-5972(1991).
RN [6]
RP SEQUENCE OF 58-86.
RX MEDLINE=89374061; PubMed=2775193;
RA Kimura H., Hitomi M., Odani S., Koide T., Arakawa M., Ono T.;
RT "Rat heart fatty acid-binding protein. Evidence that supports the
RT amino acid sequence predicted from the cDNA.";
RL Biochem. J. 260:303-306(1989).
RN [7]
RP PARTIAL SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=90032682; PubMed=2806260;
RA Kanda T., Iseki S., Hitomi M., Kimura H., Odani S., Kondo H.,
RA Matsubara Y., Muto T., Ono T.;
RT "Purification and characterization of a fatty-acid-binding protein
RT from the gastric mucosa of rats. Possible identity with heart
RT fatty-acid-binding protein and its parietal cell localization.";
RL Eur. J. Biochem. 185:27-33(1989).
RN [8]
RP PARTIAL SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=88326235; PubMed=3415652;
RA Jones P.D., Carne A., Bass N.M., Grigor M.R.;
RT "Isolation and characterization of fatty acid binding proteins from
RT mammary tissue of lactating rats.";
RL Biochem. J. 251:919-925(1988).
RN [9]
RP PARTIAL SEQUENCE.
RC TISSUE=Mammary gland;
RX MEDLINE=94162301; PubMed=8117746;
RA Nielsen S.U., Rump R., Hoejrup P., Roepstorff P., Spener F.;
RT "Differential regulation and phosphorylation of the fatty acid-
RT binding protein from rat mammary epithelial cells.";
RL Biochim. Biophys. Acta 1211:189-197(1994).
CC CC -1- FUNCTION: FAPB ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
CC CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
CC CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC CC -1- TISSUE SPECIFICITY: HEART, BUT ALSO SKELETAL MUSCLE, KIDNEY,
CC CC BRAIN AND MAMMARY GLAND.
CC CC -1- SIMILARITY: BELONGS TO THE FAPB/P2/CRBP/CRABP FAMILY OF
CC CC TRANSPORTERS.
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CC CC -----
DR EMBL; J02773; AAA41136.1;
DR EMBL; M18034; AAA41137.1;
DR PIR; A23838; A23838.
DR PIR; A27452; A27452.
DR PIR; A28197; A28197.
DR PIR; A28458; A28458.
DR PIR; A39551; A39551.
DR PIR; S06478; S06478.
DR HSP; P05413; 2HMB.

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DR InterPro: IPR000463; Fatty acid_Bp.
DR InterPro: IPR000566; Lipocln_cytFABP.
DR Pfam: PF00061; lipocalin; 1.
DR PRINTS: PR00178; FATTYACIDBP.
DR PROSITE: PS00214; FABP; 1.
DR TRANSPORT: Lipid-binding; Acetylation; Phosphorylation.
FT INIT_MET 0
FT MOD_RES 1
FT MOD_RES 19 1 ACETYLATION.
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES).
FT CONFLICT 63 S -> SN (IN REF. 3).
FT CONFLICT 69 E -> Q (IN REF. 5).
FT CONFLICT 70 F -> D (IN REF. 3).
SQ SEQUENCE 132 AA; 14643 MW; 31B4C66A8BF845BE CRC64;

Query Match 69.9%; Score 472; DB 1; Length 132;
Best Local Similarity 70.5%; Pred. No. 1.2e-35;
Matches 91; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

Qy 3 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 62
Db 2 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 61
Qy 63 ISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKREDDDKLVVECVMKG 122
Db 62 ISFQGVGEFDEVTADDRKVKSVVITLDGGKLHVQKWDGQETTLRELSDGKLILTLTHGN 121
Qy 123 VTSTRYER 131
Db 122 VVSTRYER 130

RESULT 8
FAB_MOUSE STANDARD; PRT; 132 AA.
AC P11404;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE FATTY ACID-BINDING PROTEIN, HEART (H-FABP) (MAMMARY-DERIVED GROWTH
DE INHIBITOR) (MDGI).
GN FABP3 OR FABPH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA;
RX MEDLINE=89296486; PubMed=2740224;
RA Tweedie S., Edwards Y.;
RT "cDNA sequence for mouse heart fatty acid binding protein, H-FABP."
RL Nucleic Acids Res. 17:4374-4374(1989).
RN [2]
RP REVISIONS TO 2-3.
RA Tweedie S.;
RL Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR SWISS; TISSUE=Liver;
RX MEDLINE=95011621; PubMed=7926807;
RA Treuner M., Kozak C.A., Gallahan D., Grosse R., Mueller T.;
RT "Cloning and characterization of the mouse gene encoding
mammary-derived growth inhibitor/heart-fatty acid-binding protein."
RL Gene 147:237-242(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=Mammary gland;
RX MEDLINE=93054235; PubMed=1429365;
RA Binas B., Spitzer E., Zschiesche W., Erdmann B., Kurtz A., Mueller T.,
RA Niemann C., Blenau W., Grosse R.;
RT "Hormonal induction of functional differentiation and mammary-derived
growth inhibitor expression in cultured mouse mammary gland

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RT explants.";
RL In Vitro Cell. Dev. Biol. 28A:625-634 (1992).
CC -!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
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CC -----
CC EMBL; X14961; CAA33084.1; -
CC EMBL; U02884; AAA61933.1; -
CC EMBL; U02883; AAA03445.1; -
CC PIR; S04591; S04591.
CC HSP; P05413; 2HMB.
CC SWISS-2DPAGE; P11404; MOUSE.
CC MGD; MGI:95476; Fabp3.
CC InterPro: IPR000463; Fatty acid_Bp.
CC InterPro: IPR000566; Lipocln_cytFABP.
CC Pfam: PF00061; lipocalin; 1.
CC PRINTS: PR00178; FATTYACIDBP.
CC PROSITE: PS00214; FABP; 1.
CC TRANSPORT: Lipid-binding; Acetylation; Phosphorylation.
FT INIT_MET 0
FT MOD_RES 1
FT MOD_RES 19 1 ACETYLATION (BY TYR-KINASES).
FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES).
FT CONFLICT 33 A -> G (IN REF. 1).
FT CONFLICT 98 D -> N (IN REF. 3 AND 4).
SQ SEQUENCE 132 AA; 14689 MW; F78BAE6DACIABB6A CRC64;

Query Match 69.0%; Score 466; DB 1; Length 132;
Best Local Similarity 69.0%; Pred. No. 4.1e-35;
Matches 89; Conservative 14; Mismatches 26; Indels 0; Gaps 0;

Qy 3 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 62
Db 2 DAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 61
Qy 63 ISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKREDDDKLVVECVMKG 122
Db 62 INFQGVGEFDEVTADDRKVKSLVITLDGGKLHVQKWDGQETTLRELVDGKLILTLTHGS 121
Qy 123 VTSTRYER 131
Db 122 VVSTRYER 130

RESULT 9
MYP2_HUMAN STANDARD; PRT; 131 AA.
AC P02689;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MYELIN P2 PROTEIN.
GN PMP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92068191; PubMed=1720307;
RA Hayasaka K., Nanao K., Tahara M., Sato W., Takada G., Miura M.,
RA Uyemura K.;

```

"Isolation and sequence determination of cDNA encoding P2 protein of human peripheral myelin.";
Biochem. Biophys. Res. Commun. 181:204-207(1991).
[2]
SEQUENCE.
RX MEDLINE=83058785; PubMed=6183401;
RA Suzuki M., Kitamura K., Sakamoto Y., Uyemura K.;
RT "The complete amino acid sequence of human P2 protein.";
RL J. Neurochem. 39:1759-1762(1982).
[3]
SEQUENCE OF 1-115 FROM N.A.
RX MEDLINE=95054012; PubMed=7525873;
RA Narayanan V., Ripepi B., Jabs E.W., Hawkins A., Griffin C.,
RA Tennekoon G.;
RT "Partial structure and mapping of the human myelin P2 protein gene.";
RL J. Neurochem. 63:2010-2013(1994).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN CELLS.
CC
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN PROTEIN.
CC
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPB FAMILY OF TRANSPORTERS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; D16181; BAA03726.1; JOINED.
CC EMBL; D16179; BAA03726.1; JOINED.
CC EMBL; D16180; BAA03726.1; JOINED.
CC EMBL; X62167; CAA44096.1; JOINED.
CC EMBL; X73470; AAB32592.2; JOINED.
CC EMBL; S73468; AAB32592.2; JOINED.
CC EMBL; S73469; AAB32592.2; JOINED.
CC PIR; A03143; MPB02.
CC HSSP; P02690; 1PMP.
CC JN; JT0977; JT0977.
CC MW; 170715; -.
CC InterPro; IPR000463; Fatty_acid_BP.
CC InterPro; IPR000566; Lipocalin_cytFABP.
CC Pfam; PF00061; Lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
CC Myelin; Lipid-binding; Transport; Acetylation.
CC INIT_MET 0 0
CC MOD_RES 1 1 ACETYLTATION.
CC DISULFID 117 124
CC CONFLICT 24 24 G -> GG (IN REF. 3).
CC CONFLICT 98 98 D -> N (IN REF. 2).
CC CONFLICT 110 110 N -> D (IN REF. 2).
CC SEQUENCE 131 AA; 14778 MW; 300E640BA03E69D2 CRC64;

Query Match 68.0%; Score 459; DB 1; Length 131;
Best Local Similarity 68.5%; Pred. No. 1.7e-34;
Matches 87; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 5 FVGWTKLVSSNFDDYMKVEGVGFATRKVAGMAKNMIISVNGDVITIKSESTFKNTEIS 64
1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 4 FLGTWTKLVSSNFDDYMKALGVGLATRLKGLNLAKEPRVLSKKGDIITIRTESTFKNTEIS 63

QY 65 FILGOEFDEVTDARRKVKSTITLDGGVLHVQKWDGKSTTKRKREDKLVVCEYKMGVT 124
1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 64 FKLGOEFDEVTDARRKVKSTITLDGGVLHVQKWDGKSTTKRKREDKLVVCEYKMGVT 123

QY 125 STRVYER 131
|||:|:
DB 124 CTRIYEK 130

RESULT 10
MYP2_BOVIN
ID MYP2_BOVIN STANDARD; PRT; 131 AA.
AC P02690;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MYELIN P2 PROTEIN.
GN PMP2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=80225120; PubMed=6156092;
RA Kitamura K., Suzuki M., Suzuki A., Uyemura K.;
RT "The complete amino acid sequence of the P2 protein in bovine peripheral nerve myelin.";
RL FEBS Lett. 115:27-30(1980).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=89003045; PubMed=2458918;
RA Jones T.A., Bergfors T., Sedzik J., Unge T.;
RT "The three-dimensional structure of P2 myelin protein.";
RL EMBL J. 7:1597-1604(1988).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=93253782; PubMed=7683727;
RA Cowan S.W., Newcomer M.E., Jones T.A.;
RT "Crystallographic studies on a family of cellular lipophilic transport proteins. Refinement of P2 myelin protein and the structure determination and refinement of cellular retinol-binding protein in complex with all-trans-retinol.";
RL J. Mol. Biol. 230:1225-1246(1993).
CC -!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN CELLS.
CC
CC -!- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN PROTEIN.
CC
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRAPB FAMILY OF TRANSPORTERS.
CC
CC PIR; A03144; MPB02.
CC PDB; 1PMP; 26-JAN-95.
CC InterPro; IPR000463; Fatty_acid_BP.
CC InterPro; IPR000566; Lipocalin_cytFABP.
CC Pfam; PF00061; Lipocalin; 1.
CC PRINTS; PR00178; FATTYACIDBP.
CC PROSITE; PS00214; FABP; 1.
CC Myelin; Lipid-binding; Transport; Acetylation; 3D-structure.
CC MOD_RES 1 1 ACETYLTATION.
CC DISULFID 117 124
CC SEQUENCE 131 AA; 14818 MW; 1424AAF386EA0B21 CRC64;

Query Match 66.4%; Score 448; DB 1; Length 131;
Best Local Similarity 67.7%; Pred. No. 1.6e-33;
Matches 86; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 5 FVGWTKLVSSNFDDYMKVEGVGFATRKVAGMAKNMIISVNGDVITIKSESTFKNTEIS 64
1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 4 FLGTWTKLVSSNFDDYMKALGVGLATRLKGLNLAKEPRVLSKKGDIITIRTESTFKNTEIS 63

QY 65 FILGOEFDEVTDARRKVKSTITLDGGVLHVQKWDGKSTTKRKREDKLVVCEYKMGVT 124
1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 64 FKLGOEFDEVTDARRKVKSTITLDGGVLHVQKWDGKSTTKRKREDKLVVCEYKMGVT 123

QY 125 STRVYER 131
|||:|:
DB 124 CTRIYEK 130

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RESULT 11
MYP2_MOUSE
ID MYP2_MOUSE STANDARD; PRT; 131 AA.
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE FATTY ACID-BINDING PROTEIN, HEART (H-FABP) (MUSCLE FATTY ACID-BINDING
DE PROTEIN) (M-FABP) (MAMMARY-DERIVED GROWTH INHIBITOR) (MDGI).
GN FABP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=91248148; PubMed=1710107;
RA Peeter R.A., Veerkamp J.H., Kanda T., Ono T., Geurts van Kessel A.;
RT "Cloning of the cDNA encoding human skeletal-muscle
RT fatty-acid-binding protein, its peptide sequence and chromosomal
RT localization."
RL Biochem. J. 276:203-207(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=91094793; PubMed=2266954;
RA Boerchers T., Hoejrup P., Nielsen S.U., Roepstorff P., Spener F.,
RT Knudsen J.;
RT "Revision of the amino acid sequence of human heart fatty
RT acid-binding protein."
RL Mol. Cell. Biochem. 98:127-133(1990).
RN [6]
RP SEQUENCE OF 14-132 FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=94085953; PubMed=8262516;
RA Troxler R.F., Offner G.D., Jiang J.W., Wu B.L., Skare J.C.,
RA Milunsky A., Wyandt H.E.;
RT "Localization of the gene for human heart fatty acid binding protein
RT to chromosome 1p32-1p33."
RL Hum. Genet. 92:563-566(1993).
RN [7]
RP SEQUENCE OF 31-38.
RC TISSUE=Heart;
RX MEDLINE=96007936; PubMed=7498159;
RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
RA Ershova E.S., Egorov T.A., Musalyanov A.K.;
RT "The major protein expression profile and two-dimensional protein
RT database of human heart."
RL Electrophoresis 16:1160-1169(1995).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=92406763; PubMed=1526991;
RA Zanotti G., Scapin G., Spadon P., Veerkamp J.H., Sacchettini J.C.;
RT "Three-dimensional structure of recombinant human muscle fatty acid-
RT binding protein."
RL J. Biol. Chem. 267:18541-18550(1992).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).

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DT 01-NOV-1988 (Rel. 09, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE FATTY ACID-BINDING PROTEIN, HEART (H-FABP) (MUSCLE FATTY ACID-BINDING
DE PROTEIN) (M-FABP) (MAMMARY-DERIVED GROWTH INHIBITOR) (MDGI).
GN FABP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=91248148; PubMed=1710107;
RA Peeter R.A., Veerkamp J.H., Kanda T., Ono T., Geurts van Kessel A.;
RT "Cloning of the cDNA encoding human skeletal-muscle
RT fatty-acid-binding protein, its peptide sequence and chromosomal
RT localization."
RL Biochem. J. 276:203-207(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=91094793; PubMed=2266954;
RA Boerchers T., Hoejrup P., Nielsen S.U., Roepstorff P., Spener F.,
RT Knudsen J.;
RT "Revision of the amino acid sequence of human heart fatty
RT acid-binding protein."
RL Mol. Cell. Biochem. 98:127-133(1990).
RN [6]
RP SEQUENCE OF 14-132 FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=94085953; PubMed=8262516;
RA Troxler R.F., Offner G.D., Jiang J.W., Wu B.L., Skare J.C.,
RA Milunsky A., Wyandt H.E.;
RT "Localization of the gene for human heart fatty acid binding protein
RT to chromosome 1p32-1p33."
RL Hum. Genet. 92:563-566(1993).
RN [7]
RP SEQUENCE OF 31-38.
RC TISSUE=Heart;
RX MEDLINE=96007936; PubMed=7498159;
RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
RA Ershova E.S., Egorov T.A., Musalyanov A.K.;
RT "The major protein expression profile and two-dimensional protein
RT database of human heart."
RL Electrophoresis 16:1160-1169(1995).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=92406763; PubMed=1526991;
RA Zanotti G., Scapin G., Spadon P., Veerkamp J.H., Sacchettini J.C.;
RT "Three-dimensional structure of recombinant human muscle fatty acid-
RT binding protein."
RL J. Biol. Chem. 267:18541-18550(1992).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).

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Query Match 66.1%; Score 446; DB 1; Length 131;
Best Local Similarity 66.1%; Pred. No. 2.5e-33;
Matches 84; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 5 FVGTWKLVSSENFDDYKVEGVGATRKVACMAKPNMIISVNGDVIYIKSESTFKNTEIS 64
Db 4 FLGTWKLVSSEHFDYKALGVGLANRKLNIARPTVYIISKQYDITIRTSFAFNTEIS 63
QY 65 FILGQFDEVTADNRKVKSTITLDGGVLVHVQKWDGKSTTIKKRREDKLVVECVKMGVT 124
Db 64 FKLGQFDEVTADNRKAKSVITLERSLQVKQKWDGKETAIRILLDGRVVEICMGV 123
QY 125 STRYIER 131
Db 124 CTRIYK 130
RESULT 12
FABH_HUMAN
ID FABH_HUMAN STANDARD; PRT; 132 AA.
AC P05413; Q99957;

```


KW Transport; Lipid-binding; Acetylation; Phosphorylation.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES) (BY
 FT SIMILARITY).
 SQ SEQUENCE 132 AA; 14618 MW; B5431B65EF596C95 CRC64;

Query Match 65.5%; Score 442; DB 1; Length 132;
 Best Local Similarity 65.1%; Pred. No. 5.7e-33;
 Matches 84; Conservative 15; Mismatches 30; Indels 0; Gaps 0;

Qy 3 DAFVGTWKLVSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 62
 Db 2 DAFAGTGWLVSKNFDYKMGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 61
 Qy 63 ISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKRKREDDKLVECVKMG 122
 Db 62 ISFKLGVEFDEVTADDRKVKSTITLDGGKLVLHQLKNGOETTLVRELVDGKLILTLTHGS 121
 Qy 123 VTSTRYER 131
 Db 122 AVCTRTYER 130

RESULT 15
 ID FABB_BOVIN STANDARD; PRT; 131 AA.
 AC Q09139;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE FATTY ACID-BINDING PROTEIN, BRAIN (B-FABP).
 GN FABP7.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=91094811; PubMed=2266968;
 RA Schoentgen F., Bonanno L.M., Pignede G., Jolles P.;
 RT "Amino acid sequence and some ligand binding properties of fatty
 RT acid-binding protein from bovine brain.";
 RL Mol. Cell. Biochem. 98:35-39(1990).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=90032683; PubMed=2806261;
 RA Schoentgen F., Pignede G., Bonanno L.M., Jolles P.;
 RT "Fatty-acid-binding protein from bovine brain. Amino acid sequence
 RT and some properties.";
 RL Eur. J. Biochem. 185:35-40(1989).
 CC -1- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
 CC TRANSPORT OF LONG CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
 CC BINDS OLEIC AND PALMITIC ACIDS BUT NOT PALMITOYL COA.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
 CC TRANSPORTERS.
 DR InterPro; IPR000463; Fatty_acid_BP.
 DR InterPro; IPR000566; Lipocln_cytFABP.
 DR Pfam; PF00061; lipocalin; 1.
 DR PRINTS; PR00178; FATTYACIDBP.
 DR PROSITE; PS00214; FABP; 1.
 KW Transport; Lipid-binding.
 FT VARIANT 11 12 TE -> VD.
 FT VARIANT 14 14 Q -> K.
 FT VARIANT 18 18 E -> D.
 FT VARIANT 33 34 GN -> AS.
 FT VARIANT 40 40 L -> T.

FT VARIANT 43 44 SV -> EK.
 FT VARIANT 49 49 E -> V.
 FT VARIANT 65 65 H -> K.
 FT VARIANT 68 68 E -> V.
 FT VARIANT 72 72 D -> E.
 FT VARIANT 78 78 Q -> R.
 FT VARIANT 83 83 I -> V.
 FT VARIANT 105 105 V -> T.
 FT VARIANT 108 108 M -> L.
 FT VARIANT 121 122 DV -> TA.
 FT VARIANT 127 127 H -> T.
 SQ SEQUENCE 131 AA; 14590 MW; A26FF5D63C0CF2B4 CRC64;

Query Match 63.0%; Score 425; DB 1; Length 131;
 Best Local Similarity 62.0%; Pred. No. 1.9e-31;
 Matches 80; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

Qy 3 DAFVGTWKLVSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 62
 Db 2 DAFVGTWKLVSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 61
 Qy 63 ISFILGQEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKRKREDDKLVECVKMG 122
 Db 62 ISFKLGVEFDEVTADDRKVKSTITLDGGKLVLHQLKNGOETTLVRELVDGKLILTLTHGS 121
 Qy 123 VTSTRYER 131
 Db 122 AVCTRTYER 130

Search completed: January 24, 2002, 09:18:21
 Job time: 178 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 24, 2002, 09:15:43 ; Search time 25.01 Seconds
(without alignments)
772.009 Million cell updates/sec

Title: US-09-905-235-1

Perfect score: 675

Sequence: 1 MCDAFVGTWKLVSSENFDDY.....KLVVECVMGVSTRVYERA 132

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.invertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	651	96.4	132	11 Q99P60	Q99P60 spermophilu
2	603	89.3	150	11 Q9R290	Q9R290 rattus norv
3	537	79.6	113	6 Q9XSG4	Q9XSG4 oryctolagus
4	473.5	70.1	134	11 Q9QY04	Q9QY04 rattus norv
5	468	69.3	133	11 Q99P61	Q99P61 spermophilu
6	433	64.1	99	6 Q97675	Q97675 sus scrofa
7	427	63.3	125	6 Q9XS15	Q9XS15 equus caball
8	413	61.2	132	13 Q918N9	Q918N9 brachydanio
9	402	59.6	132	11 Q9DAL2	Q9DAL2 mus musculu
10	400	59.3	133	13 Q57668	Q57668 cryodracro a
11	397	58.8	133	13 Q57667	Q57667 chaenoceph
12	397	58.8	133	13 Q57670	Q57670 gobionototh
13	393.5	58.3	134	13 Q57691	Q57691 cryodracro a
14	392	58.1	133	13 Q57669	Q57669 nototheria
15	391.5	58.0	134	13 Q57666	Q57666 paracheaenic
16	390.5	57.9	134	13 Q57665	Q57665 gobionototh
17	387.5	57.4	134	13 Q57663	Q57663 nototheria
18	384	56.9	135	13 Q91896	Q91896 anguilla ja
19	379	56.1	166	4 Q9H047	Q9H047 homo sapien

20	374	55.4	132	11 Q9DAK4	Q9DAK4 mus musculu
21	341	50.5	97	11 Q9QV90	Q9QV90 mus sp. lmg
22	307.5	45.6	135	5 Q01812	Q01812 caenorhabdi
23	300.5	44.5	136	5 Q01814	Q01814 caenorhabdi
24	285	42.2	130	5 Q9VGM2	Q9VGM2 drosophila
25	270.5	40.1	133	5 Q9BMK1	Q9BMK1 echinococcu
26	270.5	40.1	133	5 Q9BLV5	Q9BLV5 echinococcu
27	256.5	38.0	137	5 Q02323	Q02323 caenorhabdi
28	254.5	37.7	132	5 Q026517	Q026517 schistosoma
29	252	37.3	132	5 Q61236	Q61236 manduca sex
30	248.5	36.8	133	5 Q9BMK2	Q9BMK2 echinococcu
31	247.5	36.7	100	13 Q57664	Q57664 rhigophila
32	247.5	36.7	132	5 Q9BMK8	Q9BMK8 schistosoma
33	244.5	36.2	133	5 Q9BMK3	Q9BMK3 echinococcu
34	231.5	34.3	132	5 Q45035	Q45035 schistosoma
35	224	33.2	134	11 Q9EPC5	Q9EPC5 mus musculu
36	222	32.9	134	11 Q9DIN1	Q9DIN1 mus musculu
37	210	31.1	114	11 Q99M00	Q99M00 mus musculu
38	204.5	30.3	120	5 Q45036	Q45036 schistosoma
39	201.5	29.9	132	5 Q9ULG6	Q9ULG6 fasciola he
40	189.5	28.1	147	13 Q9PSA5	Q9PSA5 xenopus lae
41	184	27.3	132	13 Q9PRH9	Q9PRH9 brachydanio
42	167	24.7	176	5 Q02324	Q02324 caenorhabdi
43	165	24.4	135	4 P82980	P82980 homo sapien
44	157.5	23.3	126	13 Q918L5	Q918L5 brachydanio
45	156.5	23.2	132	5 Q9UAS2	Q9UAS2 fasciola gi

ALIGNMENTS

RESULT 1

Q99P60 PRELIMINARY; PRT; 132 AA.
AC Q99P60
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADIPOSE-TYPE FATTY ACID-BINDING PROTEIN.
GN FABP4.
OS Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Scluridae; Sclurinae;
OC Spermophilus.
OX NCBI_TaxID=43179;
RN [1]
RP SEQUENCE FROM N.A.
RA Hittel D.S., Storey K.B.;
RT "Differential expression of adipose- and heart-type fatty acid-binding proteins in hibernating ground squirrels."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF327855; AAK08084.1;
SQ SEQUENCE 132 AA; 14765 MW; FCB14230E34C0708 CRC64;

Query Match 96.4%; Score 651; DB 11; Length 132;
Best Local Similarity 97.0%; Pred. No. 51e-50;
Matches 128; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MCDAFVGTWKLVSSENFDDYMKVEGVGFATPKVAGAKPMNIISVNGDVITIKSESTFKN 60

DB 1 MCDAFVGTWKLVSSENFDDYMKVEGVGFATPKVAGAKPMNIISVNGDVITIKSESTFKN 60

QY 61 TETSFILGQEFDEVTADDRKVKSTIILDGVLVHVOKWKGKSTTIKKRDEDDKLWVECVM 120

DB 61 TETSFILGQEFDEVTADDRKVKSTIILDGVLVHVOKWKGKSTTIKKRDEDDKLWVECVM 120

QY 121 KGVSTRVYERA 132

DB 121 KGVSTRVYERA 132

RESULT 2

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Q9R290
ID Q9R290 PRELIMINARY; PRT; 150 AA.
AC Q9R290;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ADIPOCYTE LIPID-BINDING PROTEIN.
GN ALBP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=ADIPOSE TISSUE;
RX MEDLINE=9925407; PubMed=10318917;
RA Shen W.-J., Sridhar K., Bernlohr D.A., Kraemer F.B.;
RT "Interaction of rat hormone-sensitive lipase with adipocyte lipid-
binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:5528-5532(1999).
DR EMBL; AF144756; AAD37371.1; -.
DR HSP; P04117; ILLD.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytfabp.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
SQ SEQUENCE 150 AA; 16468 MW; 9D214AB610D0C54E CRC64;

Query Match 89.3%; Score 603; DB 11; Length 150;
Best Local Similarity 87.9%; Pred. No. 9.9e-46;
Matches 116; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MCDAPVGTWKLVSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVIITIKSESTFKN 60
Db 1 MCDAPVGTWKLVSSENFDDYKMGVGFATRKVAGMAKPNLIISVEGDLVIRSESTFKN 60

QY 61 TEISFILGOEFDEVTAADRKYKSTITLDGGVLHVQKWDGKSTIKRKREDDKLVEECVM 120
Db 61 TEISFKLGVFEDEITPDDRKVKSTITLDGGVLHVQKWDGKSTIKRKXGDKLVEECVM 120

QY 121 KGVSTRVYERA 132
Db 121 KGVSTRVYXRA 132

RESULT 3
Q9XSG4
ID Q9XSG4 PRELIMINARY; PRT; 113 AA.
AC Q9XSG4;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ADIPOCYTE LIPID-BINDING PROTEIN (FRAGMENT).
GN AP2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=BLADDER;
RA Guan Y., Zhang Y., Davis L., Breyer M.D.;
RT "Expression of ap2 gene in transitional epithelium of rabbit
bladder.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF136241; AAD32209.1; -.
DR HSP; P04117; ILLD.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytfabp.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.

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FT NON_TER 1 1
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12536 MW; 4C19A538EC897F4F CRC64;

Query Match 79.6%; Score 537; DB 6; Length 113;
Best Local Similarity 94.7%; Pred. No. 4.4e-40;
Matches 107; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 8 TWKLVSSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVIITIKSESTFKNTEISFIL 67
Db 1 TWKLVSSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVIITIKSESTFKNTEISFKL 60

QY 68 GQEFDEVTAADRKYKSTITLDGGVLHVQKWDGKSTIKRKREDDKLVEECVM 120
Db 61 GQEFDEVTAADRKKSIITLDGGALVQVQKWDGKSTIKRKREGDKLVEECVM 113

RESULT 4
Q9QY04
ID Q9QY04 PRELIMINARY; PRT; 134 AA.
AC Q9QY04;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE FATTY ACID-BINDING PROTEIN.
GN FABP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=HEART;
RX PubMed=10561574;
RA Zhang J., Rickers-Haunerland J., Dave I., Haunerland N.H.;
RT "Structure and chromosomal location of the rat gene encoding the heart
fatty acid-binding protein.";
RL Eur. J. Biochem. 266:347-351(1999).
DR EMBL; AF144090; AAF19003.1; -.
DR HSP; P05413; IHMT.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytfabp.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
SQ SEQUENCE 134 AA; 14888 MW; BE87C12F10992FF4 CRC64;

Query Match 70.1%; Score 473.5; DB 11; Length 134;
Best Local Similarity 70.5%; Pred. No. 2.1e-34;
Matches 93; Conservative 12; Mismatches 26; Indels 1; Gaps 1;

QY 1 MCDAPVGTWKLVSSENFDDYKMGVGFATRKVAGMAKPNMIISVNGDVIITIKSESTFKN 60
Db 1 MADAPVGTWKLVDKSNFDDYKSLGVGFATRKQVASMTPPTIIKNGDVIITIKHSTFKN 60

QY 61 TEISFILGOEFDEVTAADRKYKSTITLDGGVLHVQKWDGKSTIKRKREDDKLVEECVM 120
Db 61 TEISFQLGVFEDEVTAADRKYKSVVTLDDGKLHVQKWDGQETTLRELSDGKLILLTLT 120

QY 121 KG-VTSTRVYER 131
Db 121 HGVVSTRTYER 132

RESULT 5
Q99P61
ID Q99P61 PRELIMINARY; PRT; 133 AA.
AC Q99P61;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

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RESULT	7
Q9XS15	
ID	Q9XS15 PRELIMINARY; PRT; 125 AA.
AC	Q9XS15;
DT	01-NOV-1999 (TREMBLrel. 12, Created)
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	HEART-TYPE FATTY ACID-BINDING PROTEIN (FRAGMENT).
GN	FABP3.
OS	Equus caballus (Horse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=7796;	[1]
RN	SEQUENCE FROM N.A.
RA	Schaap F.G., Peliers M.M.A.L., Van der Vusse G.J., Glatz J.F.C.;
RL	"Cloning of equine H-FABP cDNA.";
RL	Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF143950; AAD32219.1; "
DR	HSSP; P10750; LBW.
DR	InterPro; IPR000463; Fatty_acid_BP.
DR	InterPro; IPR000566; Lipocln_cytFABP.
DR	Pfam; PF00061; lipocalin; 1.
DR	PRINTS; PR00178; FATTYACIDBP.
FT	NON_TER 1
FT	NON_TER 1
SQ	SEQUENCE 125 AA; 13965 MW; 9AF89C6A66B79D71 CRC64;
Query Match	63.3%; Score 427; DB 6; Length 125;
Best Local Similarity	66.7%; Pred. No. 2.3e-30;
Matches 82; Conservative 13; Mismatches 28; Indels 0; Gaps	
QY	9 WKLVSENEDFDYKVGVGFGATRKVAGNAKPMIISVNGDVITIKSESTFKNTSEIFSLG 68
Dd	1 WKLDISKFNDDYKIGSIGVGFGATRVANNTKPTTITEVANGDTITIKTHSTFKNTEISFKLG 60
QY	69 QEFDEVTDADRKKVKSTITLDGGVLGVHVOKDGKSTPKTKRKREDDKLVVCEVMKGVTSTRV 128
Dd	61 VEDETADRRKVKSLVDLGGKLVHVQEWNGQTLLVRELIDGKLILTLTHGSVAVSTRT 120
QY	129 YET 131
Dd	121 YEK 123
RESULT	8
Q9I8N9	
ID	Q9I8N9 PRELIMINARY; PRT; 132 AA.
AC	Q9I8N9;
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	BRAIN-TYPE FATTY-ACID BINDING PROTEIN.
OS	Brachydanio rerio (Zebrafish) (Zebra danio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopeterygii; Teleostei; Osteichthyes; Ostariophysi;
OC	Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=7955;	[1]
RN	SEQUENCE FROM N.A.
RA	TISSUE=BRAIN;
RC	Denovan-Wright E.M., Pierce M., Wright J.M.;
RL	"Nucleotide sequence of cDNA clones coding for a brain-type fatty acid
RL	binding protein and its tissue-specific expression in adult zebrafish
RL	(Danio rerio).";
RL	Biochim. Biophys. Acta 0:0-0(2000).
DR	EMBL; AF237712; AAF79948.1; "
DR	InterPro; IPR000463; Fatty_acid_BP.
DR	InterPro; IPR000566; Lipocln_cytFABP.
DR	Pfam; PF00061; lipocalin; 1.
DR	PRINTS; PR00178; FATTYACIDBP.

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
 OX Notothenioidae; Channichthyidae; Chaenoccephalus.
 RN NCBI_TaxID=36190;

[1]

RP TISSUE=HEART VENTRICLE;
 RC MEDLINE=98129752; PubMed=9461533;
 RA Vayda M.E., Londraville R.L., Cashion R.E., Costello L., Sidell B.D.;
 RT "Two distinct types of fatty acid-binding protein are expressed in
 heart ventricle of Antarctic teleost fishes.";
 RL Biochem. J. 330:375-382(1998).
 DR EMBL; U92448; AAC60356.1; -;
 DR HSSP; P10790; IBWY.
 DR InterPro; IPR000463; Fatty_acid_BP.
 DR InterPro; IPR000566; Lipocln_cytfabp.
 DR Pfam; PF00061; Lipocalin; 1.
 DR PRINTS; PR00178; FATTYACIDBP.
 SQ SEQUENCE 133 AA; 15024 MW; 85157AA2665658C3 CRC64;

Query Match 58.8%; Score 397; DB 13; Length 133;
 Best Local Similarity 57.6%; Pred. No. 1.1e-27;
 Matches 76; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

OY 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
 DB 1 MVDVFGTWNKDKSEKFEYMKKLGVGATRVQGNVTKPTTIISVEGDKVTLKQSAIKN 60
 OY 61 TEISFILGOEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECVM 120
 DB 61 TELSKLDEEFDEVTADDRKVKSEFTVDGKGLVHTQKWDGKSTSLVREVNGNSLTLTKM 120

OY 121 KGVSTRYERA 132
 DB 121 DDVESIRRYVKA 132

RESULT 12
 O57670

ID O57670 PRELIMINARY; PRT; 133 AA.
 AC O57670;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE FATTY ACID BINDING PROTEIN H8-ISOFORM.
 GN H8-FABP.

OS Gobionotothen gibberifrons.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Notoleosteoi;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
 OC Notothenioidae; Nototheniidae; Gobionotothen.
 OX NCBI_TaxID=36202;

[1]

RP TISSUE=HEART VENTRICLE;
 RC MEDLINE=98129752; PubMed=9461533;
 RA Vayda M.E., Londraville R.L., Cashion R.E., Costello L., Sidell B.D.;
 RT "Two distinct types of fatty acid-binding protein are expressed in
 heart ventricle of Antarctic teleost fishes.";
 RL Biochem. J. 330:375-382(1998).
 DR EMBL; U92451; AAC60359.1; -;
 DR HSSP; P10790; IBWY.
 DR InterPro; IPR000463; Fatty_acid_BP.
 DR InterPro; IPR000566; Lipocln_cytfabp.
 DR Pfam; PF00061; Lipocalin; 1.
 DR PRINTS; PR00178; FATTYACIDBP.
 SQ SEQUENCE 133 AA; 14997 MW; 85157AA2738C68C3 CRC64;

Query Match 58.8%; Score 397; DB 13; Length 133;
 Best Local Similarity 57.6%; Pred. No. 1.1e-27;
 Matches 76; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

OY 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
 DB 1 MVDVFGTWNKDKSEKFEYMKKLGVGATRVQGNVTKPTTIISVEGDKVTLKQSAIKN 60
 OY 61 TEISFILGOEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECVM 120
 DB 61 TELSKLDEEFDEVTADDRKVKSEFTVDGKGLVHTQKWDGKSTSLVREVNGNSLTLTKM 120
 OY 121 KGVSTRYERA 132
 DB 121 DDVESIRRYVKA 132

RESULT 13
 O57691

ID O57691 PRELIMINARY; PRT; 134 AA.
 AC O57691;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE FATTY ACID BINDING PROTEIN H6-ISOFORM.
 GN H6-FABP.

OS Cryodraco antarcticus, and
 OS Chaenoccephalus aceratus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Notoleosteoi;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
 OC Notothenioidae; Channichthyidae; Cryodraco.

NCBI_TaxID=36192, 36190;

[1]

SEQUENCE FROM N.A.

TISSUE=HEART VENTRICLE;

RA Vayda M.E., Londraville R.L., Cashion R.E., Costello L., Winnard P.,
 RA Small D.J., Hatch H., Sidell B.D.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; U92443; AAC60351.1; -;

DR EMBL; U92442; AAC60350.1; -;

DR HSSP; P10790; IBWY.

DR InterPro; IPR000463; Fatty_acid_BP.

DR InterPro; IPR000566; Lipocln_cytfabp.

DR Pfam; PF00061; Lipocalin; 1.

DR PRINTS; PR00178; FATTYACIDBP.

DR PROSITE; PS00214; FABP; 1.

SQ SEQUENCE 134 AA; 15138 MW; D4CBFC689147A98 CRC64;

Query Match 58.3%; Score 393.5; DB 13; Length 134;
 Best Local Similarity 55.4%; Pred. No. 2.2e-27;
 Matches 72; Conservative 23; Mismatches 34; Indels 1; Gaps 1;

OY 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGD-VITIKSESTFK 59
 DB 1 MVEKFGVTWKLVISSDNFDDYMKVGVGFATRVQGNRTKPNLVSVDDQGGFCLKSQSTFK 60

OY 60 NTEISFILGOEFDEVTADDRKVKSTITLDGGVLHVQKWDGKSTTIKKRREDDKLVEECV 119
 DB 61 TTEIKFLNEPFEETADDRKTKTVVTVLENGKLVQKQSWDGKSTNIERIEDGKLVAKCI 120

OY 120 MKGVSTRY 129
 DB 121 MGDVIAVRTY 130

RESULT 14
 O57669

ID O57669 PRELIMINARY; PRT; 133 AA.
 AC O57669;

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE FATTY ACID BINDING PROTEIN H8-ISOFORM.

GN H8-FABP.

OS Notothenia coriiceps neglecta (Black rockcod) (Yellowbelly rockcod).

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidae; Nototheniidae; Notothenia.
OX NCBI_TaxID=8209;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=HEART VENTRICLE;
RX MEDLINE=98129752; PubMed=9461533;
RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
RT "Two distinct types of fatty acid-binding protein are expressed in
RL heart ventricle of Antarctic teleost fishes.";
RL Biochem. J. 330:375-382(1998).
DR EMBL; U92450; AAC60358.1; -.
DR HSSP; P10790; IBWY.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
SQ SEQUENCE 133 AA; 15008 MW; 851B94538D6E78DE CRC64;

Query Match 58.1%; Score 392; DB 13; Length 133;
Best Local Similarity 56.8%; Pred. No. 3e-27;
Matches 75; Conservative 19; Mismatches 38; Indels 0; Gaps 0;

QY 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
DB 1 MVDVFGIWNKDKSEKDEYMKKLGVGATRVGNVTKPTIISVEGDKVTLKTQSAIKN 60

QY 61 TETISFILGOEFDEVTADDRKVKSTITLDGVLVHVQKWDGKSTTIKKRREDDKLVVECV 120
DB 61 TELFKLNEEFDEFTADDRKVKSPVTVDGKLVHTQKWDGKSTLVREVGNSLTILTKM 120

QY 121 KGVSTRVYERA 132
DB 121 DDVESIRRYVKA 132

RESULT 15
O57666 PRELIMINARY; PRT; 134 AA.
AC O57666;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE FATTY ACID BINDING PROTEIN H6-ISOFORM.
GN H6-FABP.
OS Parachaenichthys charcoti.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidae; Bathyracnidae; Parachaenichthys.
OX NCBI_TaxID=36187;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=HEART VENTRICLE;
RX MEDLINE=98129752; PubMed=9461533;
RA Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
RT "Two distinct types of fatty acid-binding protein are expressed in
RL heart ventricle of Antarctic teleost fishes.";
RL Biochem. J. 330:375-382(1998).
DR EMBL; U92447; AAC60355.1; -.
DR HSSP; P10790; IBWY.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
SQ SEQUENCE 134 AA; 15161 MW; D4CBFC689121AFE CRC64;
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Query Match 58.0%; Score 391.5; DB 13; Length 134;

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Best Local Similarity 55.4%; Pred. No. 3.4e-27;
Matches 72; Conservative 23; Mismatches 34; Indels 1; Gaps 1;

QY 1 MCDAFVGTWKLVSSENFDDYMKVGVGFATRKVAGMAKPNMIISVNGD-VITIKSESTFK 59
DB 1 MVEKFGVTWKNMISSDNFDDYMKVGVGFATRVGNRTKPNLVSVDDQGFVCLKSQSTFK 60

QY 60 NTEISFILGOEFDEVTADDRKVKSTITLDGVLVHVQKWDGKSTTIKKRREDDKLVVECV 119
DB 61 TTEIKFKLNEPFETTTADDRKTKVTVTLENGKLVQKOSWDGKETHIERIEDGKLVAKCI 120

QY 120 MKGVSTRVY 129
DB 121 MGDVIAVRTY 130

Search completed: January 24, 2002, 09:18:54
Job time: 191 sec
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